

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:34:32 ; Search time 1030.5 Seconds
(without alignments)
1241.095 Million cell updates/sec

Title: us-10-766-185-2

Perfect score: 20
Sequence: 1 aatgagccaccagtcgcaaa 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2296392

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBml:.*
1: gb_env:.*
2: gb_pat:.*
3: gb_ph:.*
4: gb_pl:.*
5: gb_pr:.*
6: gb_ro:.*
7: gb_sts:.*
8: gb_sy:.*
9: gb_un:.*
10: gb_vl:.*
11: gb_ov:.*
12: gb_ncg:.*
13: gb_in:.*
14: gb_om:.*
15: gb_ba:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.8	74.0	20	2	CS142282 Sequence
C 2	14.8	74.0	23	2	AX555832 Sequence
C 3	14.2	71.0	25	2	BD137038 Method of
C 4	14.2	71.0	25	2	I49790 Sequence 13
C 5	13.8	69.0	41	2	BD210966 Polyvalen
C 6	13.8	69.0	41	2	AR235363 Sequence
C 7	13.6	68.0	39	2	CQ792409 Sequence
C 8	13.6	68.0	34	2	CQ792359 Sequence
C 9	13.2	66.0	20	2	CS142185 Sequence
C 10	13.2	66.0	22	2	AR279075 Sequence
C 11	13.2	66.0	27	5	AY082793 Homo Bap1
C 12	13.2	66.0	36	6	MMPE5RNA X60865 M.musculus
C 13	13.2	66.0	39	5	HSTRK3X32 Z69494 H.sapiens m
C 14	13.2	66.0	42	2	AX555817 Sequence
C 15	13.2	66.0	48	5	HSA305425 Homo Bap1
C 16	13.2	66.0	50	2	CQ006932 Sequence
C 17	13.2	66.0	50	2	AR686596 Sequence
C 18	13	65.0	43	2	DD176025 Methods f

19	13	65.0	43	2	DD176029 Methods f
C 20	12.8	64.0	20	2	AR689610 Sequence
C 21	12.8	64.0	32	2	BD097652 A method
C 22	12.8	64.0	38	2	AR089797 Sequence
C 23	12.8	64.0	50	2	CS196297 Sequence
C 24	12.8	64.0	50	2	CS196298 Sequence
C 25	12.8	64.0	50	2	AX199554 Sequence
C 26	12.6	63.0	24	2	AX1487 Sequence 2
C 27	12.6	63.0	33	2	AX327342 Sequence
C 28	12.6	63.0	50	2	AR681179 Sequence
C 29	12.6	63.0	50	2	AX160912 Sequence
C 30	12.4	62.0	20	2	AR009483 Sequence
C 31	12.4	62.0	20	2	AR064141 Sequence
C 32	12.4	62.0	20	2	I35562 Sequence 9
C 33	12.4	62.0	20	2	AR437003 Sequence
C 34	12.4	62.0	21	2	CQ880089 Sequence
C 35	12.4	62.0	23	2	AR009484 Sequence
C 36	12.4	62.0	23	2	AR064142 Sequence
C 37	12.4	62.0	23	2	I35563 Sequence 10
C 38	12.4	62.0	24	2	A13348 Primer DNA
C 39	12.4	62.0	24	7	BX545880 Arabidops
C 40	12.4	62.0	25	2	BD139760 Ion chann
C 41	12.4	62.0	25	2	CS245405 Sequence
C 42	12.4	62.0	25	2	AR307666 Sequence
C 43	12.4	62.0	25	2	AR483522 Sequence
C 44	12.4	62.0	27	2	AX277398 Sequence
C 45	12.4	62.0	27	7	BX545749 Arabidops

ALIGNMENTS

RESULT 1
LOCUS CS142282 Sequence 243 from Patent WO2005071080. 20 bp DNA linear PAT 17-AUG-2005
DEFINITION CS142282
ACCESSION CS142282
VERSION CS142282.1 GI:73532182

KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Bhanot, S.
Modulation of glucocorticoid receptor expression
Patent: WO 2005071080-A 243 04-AUG-2005;
ISIS PHARMACEUTICALS, INC. (US)
Location/Qualifiers

FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense Compound"

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGCCACCAAGTCCAA 20
DB 19 TGAACCAACAGTCCCAA 2

RESULT 2
LOCUS AX555832 Sequence 428 from Patent WO2070755. 43 bp DNA linear PAT 27-NOV-2002
DEFINITION AX555832
ACCESSION AX555832
VERSION AX555832.1 GI:25899304

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct

other sequences; artificial sequences.

REFERENCE 1
AUTHORS Lyamichev, V. I., Kaiser, M. W. and Lyamichev, N.
TITLE Ren endonucleases
JOURNAL Patent: WO 02070755-A 428 12-SEP-2002;
Third Wave Technologies, Inc. (US)
LOCATION/Qualifiers

FEATURES
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/db_xref="taxon:32630"

ORIGIN

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGCCACCAAGTGTCCA 20
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DB 32 TGAGCCACCAAGTGTCCA 15

RESULT 3
BD137038 25 bp DNA linear PAT 18-SEP-2002
LOCUS Method of determining nucleotide sequence and protein encoded by
DEFINITION transfection into host.
ACCESSION BD137038
VERSION BD137038.1 GI:23231983
KEYWORDS JP 2002508957-A/17.
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.

REFERENCE 1 (bases 1 to 25)
AUTHORS Cioppe, G.D., Erwin, R.L., Fitzmaurice, W.P., Hanley, K.M.,
Kumagai, M.H., Lindbo, J.A., McGee, D.R., Padgett, H.S. and Pogu, G.P.
TITLE Method of determining nucleotide sequence and protein encoded by
JOURNAL transfection into host
PATENT: JP 2002508957-A 17 26-MAR-2002;
LARGE SCALE BIOLOGY CORP

COMMENT
OS VITUS
PN JP 2002508957-A/17
PD 26-MAR-2002
PF 15-JAN-1999 JP 2000540219
PR 16-JAN-1998 US 09/008186
PI GUY DELLA CIOPIA, ROBERT L ERWIN, WAYNE P
FITZMAURICE, KATHLEEN M

PI HANLEY,
PI MONTO H KUMAGAI, JOHN A LINDBO, DAVID R MCGEE, HAL S PADGETT, PI
GREGORY P POGUE
PC C12N15/09, C12N15/00, C12Q1/68//A01H1/00, C12N5/10, C12N15/00, PC
C12N15/00,
PC C12N5/00
CC Method of determining nucleotide sequence and protein encoded
CC by
CC transfection into host.
FH Key location/Qualifiers
FT source 1..25
/organism="Virus".
Location/Qualifiers

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ORIGIN

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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACCAAGTGTCCA 20
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DB 19 ATGAGCCACCAAGTGTCCA 1

RESULT 4
LOCUS 149790
DEFINITION Sequence 13 from patent US 5641661.
ACCESSION 149790
VERSION 149790.1 GI:2472010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Kumagai, M.H. and Sverlow, G.G.
TITLE Pichia pastoris alcohol oxidase ZZA1 and ZZA2 regulatory regions
JOURNAL for heterologous gene expression
PATENT: US 5641661-A 13 24-JUN-1997;
LOCATION/Qualifiers

FEATURES
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 71.0%; Score 14.2; DB 2; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.8e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACCAAGTGTCCA 20
|||||
DB 19 ATGAGCCACCAAGTGTCCA 1

RESULT 5
BD210966 41 bp DNA linear PAT 17-JUL-2003
LOCUS Polyvalent unsaturated fatty acid in plant.
DEFINITION BD210966
ACCESSION BD210966.1 GI:33020736
VERSION JP 2002517255-A/1.
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 41)
AUTHORS Knutzon, D.
TITLE Polyvalent unsaturated fatty acid in plant
JOURNAL Patent: JP 2002517255-A 1 18-JUN-2002;
CALGENE LLC

COMMENT
OS Artificial Sequence
PN JP 2002517255-A/1
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553604
PR 12-JUN-1998 US 60/089043
PI DEBBIE KNUZZON

PC C12N15/09, A01H5/00, C12P7/64, C12N15/00
CC Synthetic oligonucleotide
FH Key location/Qualifiers
FT source 1..41
/organism="Artificial Sequence".
Location/Qualifiers

FEATURES
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 69.0%; Score 13.8; DB 2; Length 41;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCT 17
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DB 34 AATGAGCCACCAAGTGTCT 18

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RESULT 6
REFERENCE AR235363/c 41 bp DNA 1linear PAT 20-DEC-2002
LOCUS AR235363
DEFINITION Sequence 3 from patent US 6459018.
ACCESSION AR235363
VERSION AR235363.1 GI:27278499
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 41)
TITL Knutzen,D.
JOURNAL Polyunsaturated fatty acids in plants
Patent: US 6459018-A 3 01-OCT-2002;
Monsanto Technology LLC; St. Louis, MO
FEATURES
source 1..41
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 69.0%; Score 13.8; DB 2; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.9e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AATGAGCCACGATGTC 17
Db 34 AATGAGCCACGATGTC 18
RESULT 7
LOCUS CQ792409 29 bp DNA 1linear PAT 29-MAR-2004
DEFINITION Sequence 154 from Patent WO2004020642.
ACCESSION CQ792409
VERSION CQ792409.1 GI:45823909
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS McCourt,P., Ghassemiian,M., Cutler,S. and Bonetta,D.
TITL Stresses tolerance and delayed senescence in plants
JOURNAL Patent: WO 2004020642-A 154 11-MAR-2004;
Performance Plants, Inc. (CA)
FEATURES
source 1..29
/location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence: PCR Primer"
ORIGIN
Query Match 68.0%; Score 13.6; DB 2; Length 29;
Best Local Similarity 80.0%; Pred. No. 5.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 AATGAGCCACGATGTC 20
Db 1 AAAGAGCTCCCAATGCCA 20
RESULT 8
LOCUS CQ792359 34 bp DNA 1linear PAT 29-MAR-2004
DEFINITION Sequence 104 from Patent WO2004020642.
ACCESSION CQ792359
VERSION CQ792359.1 GI:45823868
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
ORIGIN
Query Match 68.0%; Score 13.6; DB 2; Length 34;
Best Local Similarity 80.0%; Pred. No. 5e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 AATGAGCCACGATGTC 20
Db 1 AATGAGCTCCCAATGCCA 20
RESULT 9
REFERENCE CS142185 20 bp DNA 1linear PAT 17-AUG-2005
LOCUS CS142185
DEFINITION Sequence 146 from Patent WO2005071080.
ACCESSION CS142185
VERSION CS142185.1 GI:73532085
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS Bhanot,S.
TITL Modulation of glucocorticoid receptor expression
JOURNAL Patent: WO 2005071080-A 146 04-AUG-2005;
ISIS PHARMACEUTICALS, INC. (US)
FEATURES
source 1..20
/location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Antisense Compound"
ORIGIN
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Best Local Similarity 83.3%; Pred. No. 8.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 TGAAGCCACGATGTC 20
Db 19 TAAACCAACGATGCCCA 2
RESULT 10
REFERENCE AR279075 22 bp DNA 1linear PAT 10-APR-2003
LOCUS AR279075
DEFINITION Sequence 208 from patent US 6514694.
ACCESSION AR279075
VERSION AR279075.1 GI:29713718
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 22)
TITL Milhausen,M.J.
JOURNAL Methods for the detection of encypted parasites
Patent: US 6514694-A 208 04-FEB-2003;
Heska Corporation; Fort Collins, CO
FEATURES
source 1..22
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/mol_type="genomic DNA"
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ORIGIN

Query Match 66.0%; Score 13.2; DB 2; Length 22;
 Best Local Similarity 83.3%; Pred. No. 8.4e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCAGCAGTGTCCA 19
 |||||
 21 ATGATGCACGAGTGTCCA 4

RESULT 11
 AY082793 27 bp DNA linear PRI 08-APR-2003
 LOCUS AY082793
 DEFINITION Homo sapiens clone 101.18 T cell receptor beta chain gene, partial cds.

ACCESSION AY082793
 VERSION AY082793.1
 KEYWORDS GI:29647040
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 27)
 Lin, W.L., Flincke, J.E., Sharer, L.R., Platsoucas, C.D. and Oleszak, E.L.
 TITL E oligoclonal T cells are infiltrating the brain of children with AIDS: sequence analysis revealed high proportions of identical beta-chain T-cell receptor (TCR) transcripts
 JOURNAL Unpublished
 AUTHORS 2 (bases 1 to 27)
 Lin, W.L., Flincke, J.E., Sharer, L.R., Platsoucas, C.D. and Oleszak, E.L.
 TITL Direct Submision
 JOURNAL Submitted (07-MAR-2002) Microbiology/Immunology, Temple University School of Medicine, 3400 North Broad Street, Philadelphia, PA 19140, USA

FEATURES
 source Location/Qualifiers
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 /note="normal donor PBMC"
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 /product="T cell receptor beta chain"
 <1..>27
 /note="TCR beta; CDR3 region; contains Vbeta 22.1 Dbeta2.1
 Dbeta2.5"
 /codon_start=1
 /product="T cell receptor beta chain"
 /protein_id="AA03440.1"
 /db_xref="GI:29647041"
 /translation="CASSDQETQ"

ORIGIN

Query Match 66.0%; Score 13.2; DB 5; Length 27;
 Best Local Similarity 83.3%; Pred. No. 8.1e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAGCCACGAGTGTCCA 20
 |||||
 1 TGTGCCAGCAGTGTCCA 18

RESULT 12
 MPM5RNA 36 bp mRNA linear ROD 07-FEB-1992
 LOCUS MPM5RNA
 DEFINITION M.musculus rearranged mRNA for T cell receptor beta chain
 Vbeta13/Jbeta2.7 join.
 X60865
 ACCESSION X60865.1
 VERSION GI:53624

KEYWORDS
 SOURCE T-cell receptor beta chain; Vbeta13/Jbeta2.7 join.
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 36)
 Casanova, J.L., Romero, P., Widmann, C., Kourilsky, P. and Maryanski, J.L.
 TITL T cell receptor genes in a series of class I major histocompatibility complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium berghei nonapeptide: implications for T cell allelic exclusion and antigen-specific repertoire
 JOURNAL J. Exp. Med. 174 (6), 1371-1383 (1991)
 PUBLISHED 1836010
 2 (bases 1 to 36)
 Casanova, J.L.
 REFERENCE Direct Submission
 JOURNAL Submitted (08-JUL-1991) J.L. Casanova, Ludwig Inst for Cancer Research, Lausanne Branch, Spalinges 1066, SWITZERLAND
 H-2Kd-restricted CTL clone specific for a Plasmodium berghei circumsporozoite nonapeptide.
 COMMENT location/Qualifiers
 1..36
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c; F1 (BALB/c x C57BL6)"
 /db_xref="taxon:10090"
 /clone="PE5.1.1"
 /haplotype="H-2d/Vbeta2b"
 /cell_type="CTL clone"
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 /codon_start=1
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 /protein_id="CAA43255.1"
 /db_xref="GI:53625"
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ORIGIN

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 Best Local Similarity 83.3%; Pred. No. 7.6e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAGCCACGAGTGTCCA 20
 |||||
 1 TGTGCCAGCAGTGTCCA 18

RESULT 13
 HSTRKX32 39 bp mRNA linear PRI 05-FEB-1997
 LOCUS HSTRKX32
 DEFINITION H.sapiens mRNA for T cell receptor beta chain junctional region (clone K3-32).
 X69494
 269494.1 GI:1770615
 ACCESSION 269494
 VERSION 269494.1
 KEYWORDS diversity region; joining region; T cell receptor; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 39)
 Naserke, H.R., Durinovic-Bello, I., Seidel, D. and Ziegler, A.G.
 TITL The T-cell receptor beta chain CDR3 region of BV8S1/BJ155 transcripts in type 1 diabetes
 JOURNAL Immunogenetics 45 (2), 87-96 (1996)
 PUBLISHED 8952958


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Query Match      66.0%; Score 13.2; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 7.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 TGAGCCACCATGTCCAA 20
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Db      31 TGAGCCACCATGATTCAA 14

RESULT 15

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Search completed: May 21, 2006, 22:09:05
Job time : 1033.5 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using SW model

Run on: May 21, 2006, 21:34:08 / Search time 386 Seconds
(without alignments)
361.256 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtcgcaaa 20

Scoring table: IDENTITY NUC

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Searched: 5244920 seqs, 348612431 residues

Total number of hits satisfying chosen parameters: 5218826

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: geneseqn2000s:*
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7: geneseqn2002bs:*
8: geneseqn2003s:*
9: geneseqn2003bs:*
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15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	13	ADQ88722 Human HIF
2	20	100.0	20	13	ADQ88721 Human HIF
3	18.4	92.0	37	2	AAK78996 Human HIF-1alpha
4	18	90.0	30	13	ADT78617 HIF1alpha
5	17.4	87.0	19	14	ADZ58028 Sense sir
6	17.4	87.0	19	14	ADZ58248 Antisense
7	16.4	82.0	32	10	ABZ83188 Toxicology
8	14.8	74.0	20	14	ABZ86823
9	14.8	74.0	20	15	ABZ86823
10	14.8	74.0	20	15	ABZ86823
11	14.2	71.0	21	14	ADZ53245
12	14.2	71.0	25	2	AAK78996
13	14.2	71.0	25	2	AAK78996
14	14.2	71.0	25	2	AAK78996
15	14	70.0	20	10	ACZ58076
16	13.8	69.0	41	3	AAZ59866 C. elegans
17	13.8	69.0	41	3	AAZ59866 C. elegans
18	13.6	66.0	29	10	ADK12120 Bncpp Caa

19	13.6	68.0	29	12	ADM98488	Adm98488 Plant tra
20	13.6	68.0	29	15	AEF71319	Aef71319 Bncpp-HP-
21	13.6	68.0	29	15	AEF9792	Aef9792 CaaX pre
22	13.6	68.0	34	10	ADK1180	Adk1180 AtCP Caa
23	13.6	68.0	34	12	ADM98452	Adm98452 Plant tra
24	13.6	68.0	34	15	AEF71270	Aef71270 AtCP-HP-
25	13.6	68.0	34	15	AEF9742	Aef9742 CaaX pre
26	13.4	67.0	20	11	AEZ9517	Aez9517 SNF conta
27	13.2	66.0	20	5	ABZ5611	Abz5611 Antisense
28	13.2	66.0	20	12	ADH63395	Adh63395 Human glt
29	13.2	66.0	20	12	ADH64247	Adh64247 Human glt
30	13.2	66.0	20	12	ADH63882	Adh63882 Human glt
31	13.2	66.0	20	14	ABZ86826	Abz86826 Human glt
32	13.2	66.0	20	15	AEF79537	Aef79537 Human glt
33	13.2	66.0	21	14	ACLA5856	AcLA5856 CDH6 targ
34	13.2	66.0	21	14	ACLA5526	AcLA5526 CDH6 targ
35	13.2	66.0	21	14	ACLA5857	AcLA5857 CDH6 sirN
36	13.2	66.0	21	14	ACLA5858	AcLA5858 CDH6 sirN
37	13.2	66.0	22	2	AAK91339	AAK91339 Primer fo
38	13.2	66.0	22	4	AAK42662	AAK42662 T. gondii
39	13.2	66.0	22	10	ADG17258	Adg17258 T. gondii
40	13.2	66.0	25	9	ACK30818	ACK30818 Human mtc
41	13.2	66.0	42	6	ADZ53230	Adz53230 FEN-1 rel
42	13.2	66.0	50	4	AAI32364	AAI32364 Human SNP
43	13.2	66.0	50	6	ABZ06034	Abz06034 Human leu
44	13.2	66.0	50	12	ADP12724	Adp12724 50-mer ol
45	13.2	65.0	22	11	ADM47308	Adm47308 NOVA Olig

ALIGNMENTS

RESULT 1	ADQ88722	standard; DNA; 20 BP.
ID	ADQ88722	
XX	ADQ88722:	
AC	ADQ88722:	
XX	ADQ88722:	
DT	21-OCT-2004	(first entry)
XX		
DE	Human HIF-1 antisense oligonucleotide RX-0047.	
XX		
KW	RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;	
KW	cancer; infection; inflammation; tumour formation; ss;	
KW	antisense oligonucleotide; antisense technology.	
XX		
OS	Homo sapiens.	
XX		
PN	US2004152655-A1.	
XX		
PD	05-AUG-2004.	
XX		
PF	28-JAN-2004; 2004US-00766185.	
XX		
PR	31-JAN-2003; 2003US-0444367P.	
XX		
PA	(YOON/) YOON H.	
PA	(MAOL/) MAO L.	
PA	(LEEF/) LEE Y B.	
PA	(AHNC/) AHN C.	
PA	(JIAN/) JIANG X.	
XX		
PI	Yoon H, Mao L, Lee YB, Ahn C, JIANG X,	
XX		
DR	WPI; 2004-561492/54.	
XX		
PT	New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a	
PT	nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),	
PT	useful for inhibiting expression of HIF-1 and inducing cytotoxicity in	
XX	several cancer cells.	
XX		
PS	Claim 1; SEQ ID NO 2; 35pp; English.	
XX		

DB 8 AGTGAGCCACGAGTCCAA 27

RESULT 4
ADT78617
ID ADT78617 standard; DNA, 20 BP.
XX
AC ADT78617/
XX
DT 27-JAN-2005 (first entry)
XX
DE H191alpha cDNA, antisense oligonucleotide ISIS #298743.
XX
KM Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KM hypoxia-inducible factor 2 alpha; H191alpha; HIF2alpha;
KM hyperproliferative disorder; cancer; p53; angiogenic disorder;
KM eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KM psoriasis; atherosclerosis; smooth muscle cell proliferation;
KM blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KM ophthalmological; antiinflammatory; respiratory; vasotropic; mouse; rat;
KM phosphorothioate; se.
XX
OS Homo sapiens.
OS Mus musculus.
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone. All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX
PN US2604420393-A1.
XX
PD 04-NOV-2004.
XX
PF 21-NOV-2003; 2003US-00719370.
XX
PR 23-NOV-2002; 2002US-00304126.
XX
PA (WARD/) WARD D T.
PA (DOBI/) DOBI K W.
PA (MARCU/) MARCUSON E G.
PA (FREI/) FREIER S W.
XX
PI Ward DT, Dobie KW, Marcuson EG, Freier SM;
XX
DR WPI; 2004-774955/76.
XX
PT New antisense compound which inhibits the expression of hypoxia-inducible
PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS Claim 27; SEQ ID NO 187; 195pp; English.
XX
CC The present invention relates to antisense compounds targeted to nucleic
CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC comprises an antisense oligonucleotide that specifically hybridises with
CC the nucleic acid and inhibits the expression of HIF1alpha and/or
CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage, preferably a phosphorothioate linkage. It also
CC comprises at least one modified sugar moiety, preferably a 2'-O-

CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC comprises at least one modified nucleobase, preferably a 5-
CC methylcytosine. The antisense oligonucleotides are useful for the
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC that affects the eye. The compound is also useful for treating tumours,
CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC such as stenosis or restenosis following angioplasty. It is also useful
CC in drug discovery and target validation, and can be utilised for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC The present sequence represents an antisense oligonucleotide used in the
CC examples of the present invention.
XX
SQ Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 90.0%; Score 18; DB 13; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 24;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
CY 3 TGAGCCACGAGTCCAA 20
DB (1 TGAGCCACGAGTCCAA 18)
XX
ADT58028/c
ID ADT58028 standard; RNA, 19 BP.
XX
AC ADT58028/
XX
DT 30-JUN-2005 (first entry)
XX
DE Sense siRNA oligo that modulates human HIF1 expression Seq 156.
XX
XX ss; short interfering RNA; siRNA; gene silencing; RNA interference;
XX hypoxia inducible factor 1; cancer; hyperproliferation;
XX macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;
XX antidiabetic.
XX
OS Homo sapiens.
XX
PN WO2005035759-A2.
XX
PD 21-APR-2005.
XX
PF 20-AUG-2004; 2004WO-US027294.
XX
PR 20-AUG-2003; 2003US-0496655P.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 54US-09997777.
PR 24-MAY-2004; 54US-09996666.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Uman N, Mcswiggen J;
XX
DR WPI; 2005-306364/31.
XX
PT New chemically synthesized double stranded short interfering nucleic acid
PT molecule that directs cleavage of a hypoxia inducible factor 1 RNA via
PT RNA interference (RNAi), useful for modulating HIF1, its expression or
PT activity.
XX
PS Claim 33; SEQ ID NO 156; 189pp; English.
XX
CC This invention relates to a novel chemically synthesized double stranded

CC short interfering nucleic acid strand (siRNA). Specifically, it refers to
 CC siRNAs that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via
 CC RNA interference (RNAi). In particular, the siRNAs may include short
 CC interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)
 CC and short hairpin RNA (shRNA) molecules that are capable of mediating
 CC RNAi. The present invention describes a sense strand of a double-stranded
 CC siRNA that comprises a nucleotide sequence that is complementary to HIF1
 CC RNA or a portion thereof, and where a second strand is the complementary
 CC antisense siRNA strand. Note that the sense region is connected to the
 CC antisense region via a polynucleotide linker molecule. Accordingly, these
 CC siRNAs are useful in providing compositions for the treatment of traits,
 CC diseases and conditions that respond to modulation of HIF1 expression,
 CC namely cancer and proliferative conditions including macular
 CC degeneration, diabetic retinopathy and other conditions associated with
 CC hypoxia inducible proliferation. As such, these compositions exhibit
 CC cytostatic, ophthalmological and antidiabetic activities. This
 CC oligonucleotide sequence is a sense siRNA strand that targets human HIF1
 CC RNA to modulate expression given in an exemplification of the invention.
 XX
 SQ Sequence 19 BP; 3 A; 5 C; 6 G; 0 T; 5 U; 0 Other;
 Query Match 87.0%; Score 17.4; DB 14; Length 19;
 Best Local Similarity 94.7%; Pred. No. 49;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 AATGAGCCACCACTGTCCA 19
 19 AGTGAGCCACCACTGTCCA 1
 RESULT 6
 AD258248
 ID AD258248 standard; RNA; 19 BP.
 AC AD258248;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Antisense siRNA oligo that modulates human HIF1 expression Seq 376.
 XX
 KW ss; short interfering RNA; siRNA; gene silencing; RNA interference;
 KW hypoxia inducible factor 1; cancer; hyperproliferation;
 KW macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;
 KW antidiabetic; antisense.
 OS Homo sapiens.
 XX
 PN WO2005035759-A2.
 XX
 PD 21-APR-2005.
 XX
 PF 20-AUG-2004; 2004MO-US027294.
 XX
 PR 20-AUG-2003; 2003US-0496655P.
 PR 23-OCT-2003; 2003US-00693059.
 PR 24-NOV-2003; 2003US-00720448.
 PR 03-DEC-2003; 2003US-00727780.
 PR 14-JAN-2004; 2004US-00757803.
 PR 10-FEB-2004; 2004US-0543480P.
 PR 13-FEB-2004; 2004US-00780447.
 PR 16-APR-2004; 2004US-00826966.
 PR 30-APR-2004; 54US-09997777.
 PR 24-MAY-2004; 54US-09996666.
 XX
 PA (SIRN-) SIRNA THERAPEUTICS INC.
 XX
 PI Ueman N, Mcswigen J;
 XX
 DR WPI; 2005-306364/31.
 XX
 PT New chemically synthesized double stranded short interfering nucleic acid
 PT molecule that directs cleavage of a hypoxia inducible factor 1 RNA via
 PT RNA interference (RNAi), useful for modulating HIF1, its expression or

PT activity.
 XX
 XX Claim 33; SEQ ID NO 376; 189pp; English.
 XX
 CC This invention relates to a novel chemically synthesized double stranded
 CC short interfering nucleic acid strand (siRNA). Specifically, it refers to
 CC siRNAs that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via
 CC RNA interference (RNAi). In particular, the siRNAs may include short
 CC interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)
 CC and short hairpin RNA (shRNA) molecules that are capable of mediating
 CC RNAi. The present invention describes a sense strand of a double-stranded
 CC siRNA that comprises a nucleotide sequence that is complementary to HIF1
 CC RNA or a portion thereof, and where a second strand is the complementary
 CC antisense siRNA strand. Note that the sense region is connected to the
 CC antisense region via a polynucleotide linker molecule. Accordingly, these
 CC siRNAs are useful in providing compositions for the treatment of traits,
 CC diseases and conditions that respond to modulation of HIF1 expression,
 CC namely cancer and proliferative conditions including macular
 CC degeneration, diabetic retinopathy and other conditions associated with
 CC hypoxia inducible proliferation. As such, these compositions exhibit
 CC cytostatic, ophthalmological and antidiabetic activities. This
 CC oligonucleotide sequence is an antisense siRNA strand that targets human
 CC HIF1 RNA to modulate expression given in an exemplification of the
 CC invention.
 XX
 SQ Sequence 19 BP; 5 A; 6 C; 5 G; 0 T; 3 U; 0 Other;
 Query Match 87.0%; Score 17.4; DB 14; Length 19;
 Best Local Similarity 78.9%; Pred. No. 49;
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 1 AATGAGCCACCACTGTCCA 19
 1 AGUGAGCCACCACTGTCCA 19
 RESULT 7
 AB283188/c
 ID AB283188 standard; DNA; 32 BP.
 AC AB283188;
 XX
 DT 14-MAY-2003 (first entry)
 XX
 DE Toxicologically relevant human PCR primer #347.
 XX
 KW Toxicologically relevant gene; toxicological response; PCR primer; ss.
 KW
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2003016500-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 16-AUG-2002; 2002MO-US026514.
 PR 16-AUG-2001; 2001US-0313080P.
 PR
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 XX
 PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweizer K;
 PI Allen P;
 XX
 DR WPI; 2003-268322/26.
 XX
 PT Determining a toxicological response to an agent, useful for screening of
 PT drugs, comprises comparing the expression profile of one or more human
 PT toxic response genes to a reference gene expression profile indicative of
 PT toxicity.
 XX
 PS Claim 1; Page 129; 455pp; English.

CC The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in AB282842
 CC to AB284764, or their fragments of at least 20 nucleotides, or homologues
 CC ; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
 CC exposing cells to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals
 CC XX

SO Sequence 32 BP, 5 A; 11 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 10; Length 32;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTC 18
 DB 28 AGTAGCCACCACTGTC 11

RESULT 8
 ABB68623/c
 ABB68623 standard; DNA; 20 BP.

AB68623;

06-OCT-2005 (first entry)

Mouse glucocorticoid receptor antisense oligonucleotide SEQ ID NO:243.

antisense oligonucleotide; glucocorticoid receptor; antidiabetic;
 anorectic; diabetes; obesity; syndrome X; hyperglycemia; hyperlipidemia;
 ss; phosphorothioate; 2'-O-methoxyethyl; 2'-MOE.

Mus sp.

Key Location/Qualifiers

modified_base 1..20

/tag= a

/mod_base= OTHER

/note= "phosphorothioate backbone, all cytosine residues
 are 5-methylcytosines"

modified_base 1..5

/tag= b

/mod_base= OTHER

/note= "2'-O-methoxyethyl"

modified_base 16..20

/tag= c

/mod_base= OTHER

/note= "2'-O-methoxyethyl"

US2005164271-A1.

28-JUL-2005.

20-JAN-2005; 2005US-00039629.

20-JAN-2004; 2004US-0538173P.

03-MAR-2004; 2004US-0550191P.

XX (BHAN/) BHANOT S.
 PA (DOBI/) DOBI K W.
 PA (FREI/) FREIER S M.
 PA (DEAN/) DEAN N M.
 PA (BEN/) BENNETT C F.
 PI Bhano S, Dobie KM, Freier SM, Dean NM, Bennett CF;
 DR WPI; 2005-521414/53.

XX New antisense compound targeted to a nucleic acid molecule encoding
 PT glucocorticoid receptor, useful for modulating the expression of
 PT glucocorticoid receptor, or for treating or diagnosing, e.g. diabetes or
 PT obesity.

XX Claim 18, SEQ ID NO 243; 129pp; English.

CC The invention relates to an antisense compound 13-80 nucleobases in
 CC length targeted to a nucleic acid molecule encoding glucocorticoid
 CC receptor, where the compound is complementary to the nucleic acid
 CC molecule encoding glucocorticoid receptor, and where the compound
 CC inhibits the expression of glucocorticoid receptor mRNA. Also described:
 CC (1) a method of inhibiting the expression of glucocorticoid receptor in a
 CC cell or tissue; (2) a method of treating an animal having a disease or
 CC condition associated with glucocorticoid receptor; (3) a method of
 CC decreasing blood glucose levels in an animal; and (4) a method of
 CC preventing or delaying the onset of an increase in blood lipid levels in
 CC an animal. The compounds, compositions, and methods are useful for
 CC modulating the expression of glucocorticoid receptor. They are also
 CC useful for the diagnosis and treatment of diseases and conditions
 CC associated with glucocorticoid receptor, e.g. diabetes (Type 2), obesity,
 CC metabolic syndrome X, hyperglycemia, or hyperlipidemia. The present
 CC sequence represents a mouse glucocorticoid receptor chimeric
 CC phosphorothioate antisense oligonucleotide, which is used in an example
 CC from the present invention.

SO Sequence 20 BP, 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 14; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAACCAACCACTGCCAA 20
 DB 19 TGAACCAACCACTGCCAA 2

RESULT 9
 AEF79634/c
 ID AEF79634 standard; DNA; 20 BP.

AEF79634;

06-APR-2006 (first entry)

Mouse glucocorticoid receptor antisense oligonucleotide, SEQ:243.

Antisense therapy; obesity; anorectic; diabetes;
 non-insulin dependent diabetes; hyperglycemia; antidiabetic; syndrome X;
 hypercholesterolemia; antilipemic; metabolic; glucocorticoid receptor;
 antisense oligonucleotide; phosphorothioate; ss.

Mus musculus.

Key Location/Qualifiers

modified_base 1..20

/tag= a

/mod_base= OTHER

/note= "This oligonucleotide has a phosphorothioate
 backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
 and 3' ends, which are 5 nucleotides in length. Also all
 cytosine residues are 5-methylcytosines"

FT

XX US2006025373-A1.
 XX
 XX 02-FEB-2006.
 XX
 XX 18-AUG-2005, 2005US-00207478.
 XX
 XX 20-JAN-2004; 2004US-0538173P.
 PR 03-MAR-2004; 2004US-0550191P.
 PR 20-JAN-2005; 2005US-00039629.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bhanot S, Dobie KW, Freter SM;
 PI
 XX WPI; 2006-117670/12.
 DR
 XX New antisense compound 8-80 nucleobases in length targeted to a nucleic
 PT acid molecule encoding glucocorticoid receptor, useful for treating a
 PT disease or condition mediated by glucocorticoid expression, e.g.
 PT diabetes, or obesity.
 XX
 XX Example 13; SEQ ID NO 243; 128bp; English.
 XX
 CC The invention relates to antisense oligonucleotides targeted to the
 CC glucocorticoid receptor gene, which inhibit its expression. The invention
 CC also relates to the use of these antisense oligonucleotides in methods
 CC for inhibiting glucocorticoid receptor expression; for reducing blood
 CC glucose, triglyceride, cholesterol or insulin levels; for increasing
 CC insulin sensitivity; for inhibiting hepatic glucose output; or for
 CC reducing body fat mass. The glucocorticoid receptor (encoded on human
 CC chromosome 5q11-q13) is a ubiquitously expressed cytoplasmic member of
 CC the nuclear hormone superfamily of receptors. It is responsible for
 CC mediating the effects of glucocorticoids on various physiological
 CC functions e.g., stimulation of gluconeogenesis, decreased glucose uptake
 CC and utilization in peripheral tissues, increased glycogen deposition,
 CC suppression of immune and inflammatory responses, inhibition of cytokine
 CC synthesis, and acceleration of various developmental events. Stress-
 CC induced elevation of glucocorticoid synthesis and release can lead to
 CC adverse health effects resulting from, amongst other responses, increased
 CC ventricular workload, inhibition of inflammatory mediators, inhibition of
 CC cytokine synthesis and increased glucose production. Inhibition of
 CC glucocorticoid receptor expression may therefore be useful in the
 CC treatment of diseases resulting from glucocorticoid activity. Antisense
 CC oligonucleotides targeted to the glucocorticoid receptor gene are useful
 CC for the treatment of obesity, diabetes (particularly type 2 diabetes),
 CC metabolic syndrome X, hyperglycemia and hyperlipidemia (especially
 CC elevated blood cholesterol or triglyceride levels). The present sequence
 CC represents a phosphorothioate antisense oligonucleotide targeted to mouse
 CC glucocorticoid receptor RNA.
 XX
 XX Sequence 20 BP, 2 A, 3 C, 8 G, 7 T, 0 U, 0 Other;
 SQ
 Query Match 74.0%; Score 14.8; DB 15; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGAAGCACCAAGTCCAA 20
 Db 19 TGAACCAACAGTCCCAA 2
 RESULT 10
 ADE53245/c
 ID ADE53245 standard; DNA; 43 BP.
 XX
 AC ADE53245;
 XX
 DT 29-JUN-2004 (first entry)
 XX
 XX PEN-1 related DNA used within the scope of the invention, #379.
 DB
 XX Flap endonuclease-1, PEN-1, endonuclease, structure-specific nuclease;

KW invasive cleavage structure; thermostable; DNA polymerase; 5' nuclease;
 KM viral infection; bacterial infection; cancer; forensic analysis;
 KM paternity determination; ds.
 XX
 XX Methanocaldococcus jannaschii.
 OS
 XX WO200270755-A2.
 XX
 XX 12-SEP-2002.
 XX
 XX 15-NOV-2001; 2001WO-US044953.
 XX
 XX 15-NOV-2000; 2000US-00713601.
 PR 17-NOV-2000; 2000US-00714935.
 XX
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
 PA
 XX Lyamichev VI, Kaiseer MW, Lyamicheva N;
 PI
 XX WPI; 2002-750464/81.
 DR
 XX
 XX New composition useful for detecting and characterizing nucleic acid
 PT sequences and sequence variants for detecting the presence of viral or
 PT bacterial infections or cancer, comprises purified or chimerical PEN-1
 PT endonuclease.
 XX
 XX Example 65; SEQ ID NO 427; 871bp; English.
 XX
 CC The invention discloses a new composition (1) which comprises a purified
 CC flap endonuclease-1 (PEN-1) from e.g. *Sulfolobus solfataricus*,
 CC Pyrobaculum aerophilum or a chimerical PEN-1 endonuclease having a
 CC portion of the above endonuclease in addition to that of *Pyrococcus*
 CC horikoshii and *Aeropyrum pernix*. Also claimed is a composition comprising
 CC an isolated nucleic acid sequence encoding the endonuclease mentioned
 CC above, a composition comprising a vector having the nucleic acid sequence
 CC cited above, a composition comprising a host cell and vector cited above,
 CC a mixture comprising a first structure-specific nuclease selected from
 CC the species mentioned in composition (1), and a purified second structure
 CC specific nuclease and detecting a target sequence, comprising: (a)
 CC providing a sample suspected of containing the target sequence,
 CC oligonucleotides capable of forming an invasive cleavage structure in the
 CC presence of the target sequence, and a PEN-1 endonuclease selected from
 CC the species cited above and (b) exposing the sample to the
 CC oligonucleotides and PEN-1 endonuclease. The second structure-specific
 CC nuclease also comprises a thermostable DNA polymerase. It has a 5'
 CC nuclease derived from a DNA polymerase altered in amino acid sequence
 CC such that it exhibits reduced DNA synthetic activity from that of the
 CC wild-type DNA polymerase but retains substantially the same 5' nuclease
 CC activity of the wild-type DNA polymerase. The second structure is
 CC selected from CLEAVASE BN enzyme, CLEAVASE DA enzyme, CLEAVASE DN enzyme,
 CC CLEAVASE DV enzyme, CLEAVASE BN/thrombin enzyme, CLEAVASE TTHDN enzyme,
 CC T. aquaticus DNA polymerase, T. thermophilus DNA polymerase, E. coli Exo
 CC III and S. cerevisiae Rad1/Rad10 complex. The nucleic acid treatment kit
 CC comprises (i) and oligonucleotides capable of forming an invasive
 CC cleavage structure in the presence of a target nucleic acid. The
 CC oligonucleotides comprise: (a) a first oligonucleotide having a 5'
 CC portion complementary to a first portion of a target nucleic acid and (b)
 CC a second oligonucleotide comprising a 5' portion complementary to a
 CC second portion of the target nucleic acid downstream of and contiguous to
 CC the first portion and a 3' portion. The 3' portion of the second
 CC oligonucleotide comprises a single 3' terminal nucleotide not
 CC complementary to the target nucleic acid. Additionally, the kit has a
 CC third oligonucleotide complementary to a third portion of the target
 CC nucleic acid upstream of the first portion of the first target nucleic
 CC acid. In detecting a target sequence, the oligonucleotides and
 CC endonuclease are mixed under conditions where an invasive cleavage
 CC structure is formed between the target sequence and the oligonucleotides
 CC if the target sequence is present in the sample, where the invasive
 CC cleavage structure is cleaved by the endonuclease to form a cleavage
 CC product. The composition is useful in detecting and characterizing
 CC specific nucleic acid sequences and sequence variants which can be used
 CC in detecting the presence of viral or bacterial infections, and other
 CC diseases such as cancer. The composition may also be used in forensic

CC analysis or for paternity determinations. The sequence presented is a FEN
CC -1 related DNA used within the scope of the invention.
XX
SQ Sequence 43 BP; 12 A; 13 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 6; Length 43;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 TGAGCCACCAAGTTCGA 20
DB 32 TGAGCCACCAAGTTCGA 15

RESULT 11
AC145528/c
ID AC145528 standard; RNA; 21 BP.

XX AC145528;

XX 24-MAR-2005 (first entry)

XX CDH6 siRNA antisense sequence, SEQ ID 6600.

XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX short interfering RNA; gene silencing.

XX Synthetic.

XX WO2005001092-A2.

XX 06-JAN-2005.

XX 19-MAY-2004; 2004MO-US015645.

XX 20-MAY-2003; 2003US-0471729P.

XX (AMHP) WYETH.

XX Be X, Wei L, Slonim DK, Howes SH;

XX WPI; 2005-075568/08.

XX Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.

XX Claim 3; SEQ ID NO 6600; 113pp; English.

XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pot_sequences

XX Sequence 21 BP; 5 A; 4 C; 7 G; 0 T; 5 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 14; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATGAGCCACCAAGTTCGA 19
DB 21 AATGAGCCACCAAGTTCGA 3

RESULT 12
AAT80533/c
ID AAT80533 standard; DNA; 25 BP.

XX AAT80533;

XX 25-MAR-2003 (revised)

XX 04-NOV-1997 (first entry)

XX Pichia pastoris genomic DNA PCR primer.

XX Isozymes; genomic clone; methanol-regulated promoter; yeast; starch;
XX ethanol; regulatory region; polymerase chain reaction; ss.

XX Synthetic.

XX US5641661-A.

XX 24-JUN-1997.

XX 25-MAR-1994; 94US-00220606.

XX 25-MAR-1993; 93US-00037617.

XX 25-MAR-1993; 93US-00037618.

XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.

XX Sverlow GG, Kumagai MH;

XX WPI; 1997-340945/31.

XX Conversion of starch to ethanol using recombinant yeast - which contain
PT starch-degrading enzyme coding sequence under the control of Pichia ZZAI
PT promoter.
XX Example 6; Col 17; 46pp; English.

XX A novel method has been produced for converting starch to ethanol. The
CC method involves growing yeast cells in a culture medium, where the yeast
CC cells contain a genetic construct comprising a nucleotide sequence
CC encoding a starch-degrading enzyme under the control of a ZZAI promoter
CC (the promoter of a Pichia pastoris alcohol oxidase gene). The present
CC sequence represents a PCR primer used in the amplification of Pichia
CC pastorie genomic DNA. The ZZAI promoter can direct high-level expression
CC of the rice alpha-amylase gene in Saccharomyces cerevisiae. (Updated on
CC 25-MAR-2003 to correct PF field.)

XX Sequence 25 BP; 4 A; 6 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 2; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AATGAGCCACCAAGTTCGA 20
DB 19 AATGAGCCACCAAGTTCGA 1

RESULT 13
AAX87554/c
ID AAX87554 standard; DNA; 25 BP.

XX AAX87554;

XX 08-OCT-1999 (first entry)

XX Pichia pastoris alcohol oxidase PCR primer.

KM Gene function; protein function; alcohol oxidase; PCR; primer; AOX1 gene;
 KM ss.
 XX
 OS Synthetic.
 OS Pichia pastoris.
 XX WO9936516-A2.
 XX
 PD 22-JUL-1999.
 XX
 PF 15-JAN-1999; 99WO-US001164.
 XX
 PR 16-JAN-1998; 98US-0008186.
 XX
 PA (BIO-) BIOSOURCE TECHNOLOGIES INC.
 XX Della-Cioppa G, Erwin RL, Fitzmaurice WP, Hanley KM, Kumagai MH,
 PI Iindoo JA, McGee DR, Padgett HS, Pogue GP,
 XX WPI; 1999-458459/38.
 XX
 PT Determining the function of polynucleotide sequences and their encoded
 PT proteins by transfecting them into a host organism.
 XX
 PS Example 8; Page 57; 156pp; English.
 XX
 CC This primer corresponds to the nucleotide sequence of the Pichia pastoris
 CC alcohol oxidase AOX1 gene promoter. It was used in the PCR amplification
 CC of P. pastoris cDNA. Expression in transfected Nicotiana benthamiana
 CC plants confirmed that the yeast cDNA encoded alcohol oxidase. The
 CC invention provides methods for rapidly determining the function of
 CC nucleic acid sequences by transfecting them into a host organism to
 CC effect expression, and analyzing the resulting phenotypic and biochemical
 CC changes. Methods for silencing endogenous genes, for selecting desired
 CC functions of RNAs and proteins, and for inhibiting an endogenous process
 CC in a plant host are also provided
 XX
 SQ Sequence 25 BP; 4 A; 6 C; 6 G; 9 T; 0 U; 0 Other;
 XX
 QY Query Match 71.0%; Score 14.2; DB 2; Length 25;
 Best Local Similarity 84.2%; Pred. No. 2.3e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 DB 2 ATGAGCCACCAAGTGTCCA 20
 19 ATGAGCCACCAAGTGTCCA 1
 XX
 RESULT 14
 ACP58076/c
 ID ACP58076 standard; DNA; 20 BP.
 XX
 AC ACP58076;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human PRDX3 gene fragment C Chip analysis 5' primer.
 XX
 KM PRDX3; tumour; peroxiredoxin 3; cytosolic; gene therapy; Chip analysis;
 KM Chromatin immunoprecipitation; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087312-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 08-APR-2003; 2003WO-US010539.
 XX
 PR 08-APR-2002; 2002US-0370873P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX

PI Dang CV, Monsey D;
 XX
 DR WPI; 2003-845314/78.
 XX
 PT Inhibiting tumor growth by delivering to a tumor cell, expressing an mRNA
 PT molecule complementary to native Peroxiredoxin 3 (PRDX3) mRNA, an
 PT antisense construct comprising 15 or 19 nucleotides of a murine or human
 PT PRDX3 cDNA.
 XX
 PS Claim 24; Page 23; 0pp; English.
 XX
 CC The invention relates to inhibiting tumour growth. The method involves
 CC delivering to a tumour cell an antisense construct comprising at least 15
 CC or 19 nucleotides of a murine or human Peroxiredoxin 3 (PRDX3) cDNA,
 CC where the tumour cell expresses an mRNA molecule that is complementary to
 CC native PRDX3 mRNA. The method is useful for inhibiting tumour growth.
 CC Sequences ACP58074-91 represent primers used in real-time PCR for Chip
 CC (Chromatin Immunoprecipitation) analysis of human PRDX3 genomic DNA
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
 XX
 QY Query Match 70.0%; Score 14; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 DB 4 GAGCCACCAAGTGTTC 17
 18 GAGCCACCAAGTGTTC 5
 XX
 RESULT 15
 ID ADG77414/c
 ADG77414 standard; DNA; 24 BP.
 XX
 AC ADG77414;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Canine disease marker-related PCR primer 258.
 XX
 KM genetic disease; genetic trait; dog; carrier of recessive disease;
 KM copper toxicosis; CT; canine genome map; breed-specific profile;
 KM DNA fingerprint; dog identification; PCR; primer; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9731011-A1.
 XX
 PD 28-AUG-1997.
 XX
 PF 18-FEB-1997; 97WO-US002396.
 XX
 PR 22-FEB-1996; 96US-0012060P.
 XX
 PA (UNMI) UNIV MICHIGAN.
 PA (UNMS) UNIV MICHIGAN STATE.
 XX
 PI Brewer GU, Venta PJ, Yuzbasyan-Gurkan V;
 XX
 DR WPI; 1997-435082/40.
 XX
 PT New oligonucleotide primers for diagnosis of genetic diseases and traits
 PT in dogs - amplify specific regions of the genome containing
 PT microsatellite repeats, especially for diagnosing copper toxicosis and
 PT carriers.
 XX
 PS Claim 1; Page 14; 40pp; English.
 XX
 CC This invention relates to novel oligonucleotide PCR primers which may be
 CC used to identify markers associated with genetic diseases and traits in
 CC dogs, in particular to diagnose genetic diseases that are not
 CC phenotypically visible and to identify carriers of recessive diseases. A
 CC specific application is diagnosis of copper toxicosis (CT). The invention

CC can also be used to create a genetic map of the canine genome; to
 CC generate breed-specific profiles; to establish paternity and to identify
 CC dogs from DNA fingerprints. The method provides rapid analysis of the
 CC target sequences from only a small sample of DNA. Diagnosis can be done
 CC at any time in the dog's life. The present sequence is that of a PCR
 CC primer of the invention.

XX Sequence 24 BP; 6 A; 3 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAGT 14

Db 20 AATGAGCCACCAGT 7

Search completed: May 21, 2006, 22:31:24
 Job time : 388 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:49:17 ; Search time 2196 Seconds
(without alignments)
509.284 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20
Sequence: 1 aatgagccaccagtgccaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 194034

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_g8a1:*
12: gb_g8a2:*
13: gb_g8a3:*
14: gb_g8a4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.6	68.0	50	1	AU104418 AU104418
C 2	13.6	68.0	50	12	CC571047 CH240_446
C 3	13.2	66.0	47	11	AZ588937 IM0397M06
C 4	13.2	66.0	50	10	DY245677 CSTBQ1D11
C 5	12.8	64.0	19	11	AZ601003 IM0419M06
C 6	12.8	64.0	46	2	BG389655 602415I01
C 7	12.8	64.0	46	2	BG389735 602415I01
C 8	12.6	63.0	49	13	CLS18330 DNE1D11 F
C 9	12.2	61.0	35	13	CZ194627 PST2762-N
C 10	12.2	61.0	38	11	AZ438336 IM0228E19
C 11	12	60.0	40	1	AI689673 tx95h04.x
C 12	12	60.0	46	1	AI658872 me48b09.x
C 13	12	60.0	49	1	AI629100 wj38f09.x
C 14	12	60.0	50	13	CM273788 104_746_1
C 15	11.8	59.0	30	10	TS1051 yb71d09.x
C 16	11.8	59.0	33	10	T89682 yd9f02.x
C 17	11.8	59.0	37	1	AA984865 am62b07.x
C 18	11.8	59.0	37	1	AI327021 m94f07.x
C 19	11.8	59.0	42	10	DY243241 CSTBP1802

20	11.8	59.0	46	1	AA109130	AA109130 mp38h07.x
C 21	11.8	59.0	49	1	AA995990	AA995990 os13h03.s
C 22	11.8	59.0	49	1	AI453675	AI453675 c128h04.x
C 23	11.6	58.0	29	14	AG188890	AG188890 Pan t10g1
C 24	11.6	58.0	40	1	AI318261	AI318261 tb03a09.x
C 25	11.6	58.0	42	11	AZ687147	AZ687147 2M0177E21
C 26	11.6	58.0	46	14	TA121G07Q	AL463047 T. brucei
C 27	11.4	57.0	23	5	CF298913	CF298913 71EAF--02
C 28	11.4	57.0	37	10	W70797	W70797 me44b08.r1
C 29	11.4	57.0	41	1	AA679912	AA679912 ac85c06.s
C 30	11.4	57.0	47	11	AZ783950	AZ783950 2M026D08
C 31	11.4	57.0	47	14	CT178809	CT178809 Sue scroff
C 32	11.4	57.0	50	14	CR175859	CR175859 Forward s
C 33	11.2	56.0	30	11	AZ503721	AZ503721 IM0343A11
C 34	11.2	56.0	31	14	TA216A03Q	AL479849 T. brucei
C 35	11.2	56.0	35	11	AZ308154	AZ308154 IM0010D19
C 36	11.2	56.0	35	14	BX893619	BX893619 Arabidops
C 37	11.2	56.0	38	14	TA170A06Q	AL474162 T. brucei
C 38	11.2	56.0	40	14	BX124349	BX124349 Danio rer
C 39	11.2	56.0	42	12	CC885727	CC885727 SALK 1477
C 40	11.2	56.0	43	13	CL882875	CL882875 GC0096.T1
C 41	11.2	56.0	44	11	AZ598581	AZ598581 IM0413P22
C 42	11.2	56.0	47	10	DY246292	DY246292 CSTBQ1E02
C 43	11.2	56.0	49	7	AV960480	AV960480 AV960480
C 44	11.2	56.0	50	1	AU106035	AU106035 AU106035
C 45	11.2	56.0	50	2	BG370398	BG370398 na133a04.

ALIGNMENTS

RESULT 1	AU104418/c	50 bp	RNA	linear	EST 28-JAN-2004
LOCUS	AU104418				
DEFINITION	AU104418 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone				
ACCESSION	HEP22673, mRNA sequence.				
VERSION	AU104418.1 GI:13553939				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 50)				
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Osa,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.				
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites				
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)				
COMMENT	11375929				
FEATURES	Location/Qualifiers				
source	1..50				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="HEP22673"				
ORIGIN	/clone_lib="Sugano Homo sapiens cDNA library"				
Query Match	68.0%; Score 13.6; DB 1; Length 50;				

Best Local Similarity 80.0%; Pred. No. 8.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCAA 20
DB 35 AATGAGCCACCACTGTCCAA 16

RESULT 2

CC571047/c 50 bp DNA linear GSS 18-JUN-2003
LOCUS CH240_446F14.T7 CHORI-240 Bos taurus genomic clone CH240_446F14,
DEFINITION genomic survey sequence.

ACCESSION CC571047
VERSION CC571047.1 GI:31908316
KEYWORDS GSS.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 50)
Holt, R., Scott, J., Yang, G., Barber, S., Smalhus, D., Prabhhu, A.-L.,
Teal, M., Cloutier, A., Lee, D., Gilm, N., Olson, T., Mayo, M.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
Mathewson, C., Wye, N., Maason, A., Brown-John, M., Jones, S.,
Schein, J., Marra, M., de Jong, P., Keeler, J. W., and Kappe, S. M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Unpublished (2003)
Other GSSs: CH240_446F14.TARBACT3P2

TITLE Sequencing
JOURNAL The British Columbia Cancer Agency Genome Science Centre
COMMENT 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rtholt@bccsc.ca

Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBM) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 446 Row: F Column: 14
Seq primer: T7
Class: BAC ends.

FEATURES
source Location/Qualifiers

1..50
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_446F14"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: PTARBACT.3; Site 1: MboI; Site 2: MboI;
Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 68.0%; Score 13.6; DB 12; Length 50;

Best Local Similarity 80.0%; Pred. No. 8.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCAA 20
DB 29 AATGAGCCACCACTGTCCAA 10

RESULT 3

AZ588937/c 47 bp DNA linear GSS 13-DEC-2000
LOCUS 1M037M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M037M06 R, genomic survey sequence.

ACCESSION AZ588937
VERSION AZ588937.1 GI:11711127
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 47)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0397 Row: M Column: 06
Seq primer: CACACGAGAAACAGCATGACAC
Class: plasmid ends
High quality sequence stop: 47.
Location/Qualifiers

FEATURES
source Location/Qualifiers

1..47
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M037M06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF193072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 66.0%; Score 13.2; DB 11; Length 47;

Best Local Similarity 83.3%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AATGAGCCACCACTGTCCA 19
DB 38 AATGAGCCACCACTGTCCA 21

RESULT 4
DY245677/c 50 bp mRNA linear EST 06-FEB-2006
LOCUS CSTB01D1177A_0_50 CST-BM Mus musculus cDNA, mRNA sequence.
DEFINITION DY245677
VERSION DY245677.1 GI:86581321
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)
Bowman,T.V., McCooley,A.J., Merchant,A.A., Ramos,C.A., Fonseca,P.,
Poldinger,A., Bradfield,S.B., Oliveira,D.M., Green,R., Zheng,Y.,
Jackson,K.A., Chambers,S.M., McKinney-Freeman,S.L., Norwood,K.G.,
Darlington,G., Gunaratne,P.H., Steffen,D. and Goodell,M.A.
Differential mRNA Processing in Hematopoietic Stem Cells
Stem Cells (2006) In press
Contact: Goodell MA
Center for Cell and Gene Therapy
Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713 798 1265
Fax: 713 798 1230
Email: goodell@bcm.edu.
location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_1lb="CST-BM"
/note="Organ: Bone Marrow; A hematopoietic stem cell gene
depleted library prepared by suppression subtractive
hybridization of whole bone marrow cells subtracted with
side population cells from bone marrow. Prepared as a
control for the CST-HSC library. cDNAs were fragmented,
concatenated, cloned, sequenced, and electronically
de-concatenated."

ORIGIN
Query Match 66.0%; Score 13.2; DB 10; Length 50;
Best Local Similarity 83.3%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 TGAGCCACCACTGTCCAA 20
|||||
24 TGAGGACCCCGTGACCAA 7
Db

RESULT 5
AZ601003 19 bp DNA linear GSS 13-DEC-2000
LOCUS IM0419M06F Mouse 10kb plasmid UGCLM library Mus musculus genomic
DEFINITION clone UGCLM0419M06 F, genomic survey sequence.
VERSION AZ601003
ACCESSION AZ601003.1 GI:11723193
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Ielam,H., Longacre,S., Mahmoud,M., Meenan,B., Pedersen,T.,
Ridley,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0419 row: M column: 06
Seq primer: CATTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0419M06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCLM library"
/note="Vector: pMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 64.0%; Score 12.8; DB 11; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ATGAGCCACCACTGTCT 17
|||||
Db 1 ATGACACACCACTGTCT 16

RESULT 6
BG389655 46 bp mRNA linear EST 12-MAR-2001
LOCUS 602415001P1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4523400 5',
DEFINITION mRNA sequence.
VERSION BG389655
ACCESSION BG389655.1 GI:13283103
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 46)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)

DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM10426 row: a column: 01
 High quality sequence stop: 46.
 Location/Qualifiers

FEATURES

source

1. 46
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4523400"
 /issue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH MGC 92"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC library."

ORIGIN

Query Match 64.0%; Score 12.8; DB 2; Length 46;
 Best Local Similarity 87.5%; Pred. No. 2e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AATGAGCCACCATGT 16
 |||||
 3 ACTGAGCCACCATGT 18

RESULT 7 46 bp mRNA linear EST 12-MAR-2001
 BG389736
 LOCUS 60241510F1 NIH_MGC_92 Homo sapiens cDNA IMAGE:4523401 5',
 DEFINITION mRNA sequence.
 ACCESSION BG389736 GI:13283172
 VERSION BG389736.1 GI:13283172
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 46)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM10426 row: a column: 02
 High quality sequence stop: 46.
 Location/Qualifiers

FEATURES

source

1. 46
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4523401"
 /issue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH MGC 92"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC library."

ORIGIN

Query Match 64.0%; Score 12.8; DB 2; Length 46;
 Best Local Similarity 87.5%; Pred. No. 2e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AATGAGCCACCATGT 16
 |||||
 3 ACTGAGCCACCATGT 18

RESULT 8 49 bp DNA linear GSS 02-APR-2004
 CL518330
 LOCUS DAB1011 Planking Sequence Tag of Oryza sativa T-DNA insertion lines
 DEFINITION Oryza sativa (japonica cultivar-group) genomic, genomic survey
 sequence.
 ACCESSION CL518330
 VERSION CL518330.1 GI:46145130
 KEYWORDS GSS.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BRP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 49)
 Salland,C., Gay,C., Larmande,P., Bes,M., Piffanel,J.P., Piegue,B.,
 Droc,G., Regad,F., Bourgeois,E., Neyraud,D., Petit,C.,
 Ghesquiere,A., Delzeny,M., Glaesmann,J.C. and Guiderdoni,E.
 High throughput T-DNA insertion mutagenesis in rice: A first step
 towards in silico reverse genetics
 plant J. (2004) In press
 Contact: Guiderdoni
 UMR PIA Biotop program
 CIRAD
 TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
 Tel: 33467615629
 Fax: 33467615605
 Email: emmanuel.guiderdoni@cirad.fr
 Class: TDNA tagged.
 Location/Qualifiers

FEATURES

source

1. 49
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone_1lb="Flanking Sequence Tag of Oryza sativa T-DNA
 insertion lines"
 /note="PCR was performed on DNA of primary transformants
 of Oryza sativa plants. The DNA fragment(s) resulting of
 PCR were directly sequenced from the left border to
 determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed. Information to order
 the corresponding mutant line and a link to a database
 providing a graphical display is available from June 2004
 at <http://genoplante-info.infobiogen.fr/oryzatagline/>.
 This sequence has been generated in the framework of the
 French plant genomics program Genoplante
 (<http://www.genoplante.org>) and
<http://genoplante-info.infobiogen.fr/>."

ORIGIN

Query Match 63.0%; Score 12.6; DB 13; Length 49;
 Best Local Similarity 78.9%; Pred. No. 2.6e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AATGAGCCACCATGTCCA 19
 |||||
 DB 11 AATGAGCCACCATGTACA 29

RESULT 9
 CZ194627/c

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0228 row: E column: 19
Seq primer: CGTGTGTAACAGCGCCACGT
Class: plasmid end
High quality sequence stop: 38.
Location/Qualifiers
1. 38
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U9CJM0228E19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lid="Mouse 10kb plasmid U9CJM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www.bio.linn.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -400P from Gibco
 High quality sequence stop: 1.

FEATURES

source

1. 40
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2277367"
 /tissue_type="serous papillary carcinoma, high grade, 2
 pooled tumors"
 /lab_host="DH10B"
 /clone_1lb="NCI_CGAP_Ut4"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Salt;
 Site_2: Not; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.48 kb. Life Technologies catalog #:
 11542-016"

ORIGIN

Query Match 60.0%; Score 12; DB 1; Length 40;
 Best Local Similarity 75.0%; Pred. No. 5e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATGAGCCACGATGTCGCA 20
 16 AAGGAGCCAAAGGTCGCA 35

Db

RESULT 12

AA165872

LOCUS 46 bp mRNA 1linear EST 19-DEC-1996
 DEFINITION me48509.t1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus
 CDNA clone IMAGE:614777 5' similar to TR:G295543 G295543 AFRICAN
 CLAIMED FROG BETA-TRCP. ; mRNA sequence.

ACCESSION AA165872
 VERSION AA165872.1 GI:1744331
 EST.

KEYWORDS Mus musculus (house mouse)
 SOURCE

ORGANISM Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 46)
 Martel,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Stepcie,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

REFERENCE

AUTHORS

TITLE The WashU-HMT Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMT Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LINL; contact the
 IMAGE Consortium (info@image.linn.gov) for further information.
 MGI:375601
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28M13 rev1 from Amerham

TITLE

JOURNAL

COMMENT

COMMENT

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LINL; contact the
 IMAGE Consortium (info@image.linn.gov) for further information.
 MGI:375601
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28M13 rev1 from Amerham

High quality sequence stop: 1.
 Location/Qualifiers
 1. 46
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:614777"
 /tissue_type="embryo"
 /dev_stage="13.5dpc embryos"
 /lab_host="DH10B"
 /note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1:
 Salt; Site_2: Not; Cloned unidirectionally. Primer:
 Oligo dt. 13.5dpc embryos. pCMV-SPORT2 vector."

FEATURES

source

1. 46
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:614777"
 /tissue_type="embryo"
 /dev_stage="13.5dpc embryos"
 /lab_host="DH10B"
 /note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1:
 Salt; Site_2: Not; Cloned unidirectionally. Primer:
 Oligo dt. 13.5dpc embryos. pCMV-SPORT2 vector."

ORIGIN

Query Match 60.0%; Score 12; DB 1; Length 46;
 Best Local Similarity 75.0%; Pred. No. 5.1e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATGAGCCACGATGTCGCA 20
 17 ATTGAGCAATAGATGTCGCA 36

Db

RESULT 13
 LOCUS 49 bp mRNA 1linear EST 21-DEC-1999
 DEFINITION wj38f09.x1 NCI CGAP Lul9 Homo sapiens CDNA clone IMAGE:2405129 3'
 similar to SW:ADP2_HUMAN P30041 ANTIOXIDANT PROTEIN 2 ; mRNA
 sequence.

ACCESSION A1829100.1 GI:5449771
 VERSION A1829100
 EST.

KEYWORDS Homo sapiens (human)
 SOURCE

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE 1 (bases 1 to 49)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Benito Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www.bio.linn.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 2063 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 1.

Location/Qualifiers
 1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
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 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
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 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
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 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
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 /dev_stage="adult"
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 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
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 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

1. 49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2405129"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NCI_CGAP_Lul9"
 /note="Organ: lung; Vector: pT7T3D-Paci; 1st strand CDNA

was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 60.0%; Score 12; DB 1; Length 49;
Best Local Similarity 100.0%; Pred. No. 5.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACCAAGTCCA 19
|||
24 CACCAAGTCCA 13

RESULT 14
CM273788 50 bp DNA linear GSS 31-OCT-2004
LOCUS 104.746.11404087.148.35366.024 Sorghum methylation filtered library
DEFINITION (LbID: 104) Sorghum bicolor genomic clone 11404087, genomic survey
sequence.

ACCESSION CM273788
VERSION CM273788.1 GI:54989976
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 50)

AUTHORS Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holman, H., Roe, B.A., Wiley, G., Korf, I.P., Rabinowicz, P.D., Lakey, N., McComble, W.R., Jeddeloh, J.A. and Martensen, R.A.
Sorghum genome sequencing by methylation filtration
Proc Biol. 3 (1), e13 (2005)

TITLE JOURNAL PUBLISHED
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 746 row: 1 column: 07
Seq primer: SMfor Forward
Class: methylation filtered
High quality sequence stop: 50.

FEATURES
source
1. 50
Location/Qualifiers

/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cul_tivar="RTx623"
/db_xref="taxon:4558"
/clone_1b="11404087"
/clone_1b="Sorghum methylation filtered library (LbID: 104)"
/note="Organ: leaf; Vector: pBCSK(-); Site 1: HindIII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HindIII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

Query Match 60.0%; Score 12; DB 13; Length 50;
Best Local Similarity 75.0%; Pred. No. 5.2e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATGAGCCACGATGTCGA 20

Db

31 AGTACGACTACTCTTCCA 12

RESULT 15
LOCUS T51051

DEFINITION T51051 30 bp mRNA linear EST 06-FEB-1995
YP71009.r1 Stragene ovary (#937217) Homo sapiens cDNA clone
IMAGE:76625.5, similar to gp:K16865 ELONGATION FACTOR
1-ALPHA 1 (HUMAN), mRNA sequence.

ACCESSION T51051
VERSION T51051.1 GI:652911
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 30)

REFERENCE Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE JOURNAL PUBLISHED
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 576
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LNU This clone is available royalty-free through LNU; contact the IMAGE Consortium (info@image.lnu.gov) for further information.
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FEATURES
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1. 30
Location/Qualifiers

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/db_xref="taxon:9606"
/clone="IMAGE:76625"
/sex="female"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_1b="Stragene ovary (#937217)"
/note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGACG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

ORIGIN

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Best Local Similarity 86.7%; Pred. No. 6.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGAGCCACGATG 15
|||
Db 2 AATGAGCCACGATG 16

Search completed: May 21, 2006, 23:02:45
Job time : 2200 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: May 21, 2006, 22:08:44 / Search time 115.5 Seconds
(without alignments)
324.002 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccacagtgccaa 20

Scoring table: IDENTITY_NUC

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1429044

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	14	70.0	25	3	US-09-396-196G-97802
4	14	70.0	25	3	US-09-396-196G-97803
5	14	70.0	25	3	US-09-396-196G-97804
6	14	70.0	25	3	US-09-396-196G-97805
7	13.8	69.0	41	3	US-09-330-235-3
8	13.4	67.0	25	3	US-09-396-196G-99591
9	13.4	67.0	25	3	US-09-396-196G-99592
10	13.4	67.0	25	3	US-09-396-196G-99593
11	13.2	66.0	20	3	US-09-661-753-66
12	13.2	66.0	22	3	US-09-316-392B-208
13	13.2	66.0	25	3	US-09-396-196G-60900
14	13.2	66.0	25	3	US-09-396-196G-60901
15	13.2	66.0	50	5	US-10-131-827-6025
16	13.2	66.0	50	5	US-10-131-831-6025
17	13	65.0	25	3	US-09-396-196G-97819
18	12.8	64.0	20	3	US-10-131-827-9040
19	12.8	64.0	25	3	US-09-396-196G-50633
20	12.8	64.0	25	3	US-09-396-196G-57705
21	12.8	64.0	25	3	US-09-396-196G-114077
22	12.8	64.0	25	3	US-09-396-196G-114078
23	12.8	64.0	25	3	US-09-396-196G-114079

24	12.8	64.0	25	3	US-09-396-196G-115388	Sequence 115388,
25	12.8	64.0	38	2	US-08-857-946-79	Sequence 79, Appl
26	12.8	64.0	38	3	US-08-970-740-79	Sequence 10994, A
27	12.6	63.0	25	3	US-09-396-196G-10994	Sequence 10989, A
28	12.6	63.0	25	3	US-09-396-196G-10084	Sequence 10084,
29	12.6	63.0	25	3	US-09-396-196G-10389	Sequence 10389,
30	12.6	63.0	25	3	US-09-396-196G-10389	Sequence 10389,
31	12.6	63.0	25	3	US-09-396-196G-10389	Sequence 10389,
32	12.6	63.0	50	5	US-10-131-827-608	Sequence 608, App
33	12.6	63.0	50	5	US-10-131-831-608	Sequence 608, App
34	12.4	62.0	20	2	US-08-116-389-9	Sequence 9, Appl1
35	12.4	62.0	20	2	US-08-708-431-9	Sequence 9, Appl1
36	12.4	62.0	20	2	US-08-880-830-9	Sequence 9, Appl1
37	12.4	62.0	20	3	US-09-660-473-55	Sequence 55, Appl
38	12.4	62.0	20	7	PCT-US94-13895-9	Sequence 9, Appl1
39	12.4	62.0	22	3	US-08-855-910-34	Sequence 34, Appl
40	12.4	62.0	23	2	US-08-116-389-10	Sequence 10, Appl
41	12.4	62.0	23	2	US-08-708-431-10	Sequence 10, Appl
42	12.4	62.0	23	2	US-08-880-830-10	Sequence 10, Appl
43	12.4	62.0	23	7	PCT-US94-13895-10	Sequence 13, Appl
44	12.4	62.0	25	3	US-08-997-685A-13	Sequence 1, Appl1
45	12.4	62.0	25	3	US-09-086-436-1	

ALIGNMENTS

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RESULT 1
US-09-579-897-2
; Sequence 2, Application US/09579897
; Patent No. 6432927
; GENERAL INFORMATION:
; APPLICANT: Gregory, Richard
; APPLICANT: Vincent, Karen
; TITLE OF INVENTION: Compositions and Methods for Inducing Gene Expression
; FILE REFERENCE: GA0112CIP2
; CURRENT APPLICATION NUMBER: US/09/579,897
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/067,546
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/25753
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 09/133,612
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-579-897-2

Query Match          92.0%; Score 18.4; DB 3; Length 37;
Best local similarity 95.0%; Pred. No. 3.5;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AATGACCAACAGTGCCAA 20
Db      8 AATGACCAACAGTGCCAA 27

RESULT 2
US-08-220-606B-13/c
; Sequence 13, Application US/08220606B
; Patent No. 5641661
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Monto H.
; APPLICANT: Genadi, Sverlow J.
; TITLE OF INVENTION: Pichia Pastoris Alcohol Oxidase Z2A1 and
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Penite & Edmonds
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,606B
FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halliuh, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8129-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
US-08-220-606B-13

Query Match 71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACGAGTGTCCA 20
DB 19 ATGAGCCACGAGTGTCCA 1

RESULT 3
US-09-396-196G-97802/c
Sequence 97802, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97802
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-97802

Query Match 70.0%; Score 14; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCACCAAGTGTCCA 19
DB 25 GCCACCAAGTGTCCA 12

RESULT 4

US-09-396-196G-97803/c
Sequence 97803, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97803
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-97803

Query Match 70.0%; Score 14; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCACCAAGTGTCCA 19
DB 23 GCCACCAAGTGTCCA 10

RESULT 5
US-09-396-196G-97804/c
Sequence 97804, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97804
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-97804

Query Match 70.0%; Score 14; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCACCAAGTGTCCA 19
DB 22 GCCACCAAGTGTCCA 9

RESULT 6
US-09-396-196G-97805/c
Sequence 97805, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97805
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-97805

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCACGAGTGTCCA 19
DB 20 GCCACGAGTGTCCA 7

RESULT 7
US-09-330-235-3/C
Sequence 3, Application US/09330235
Patent No. 6459018
GENERAL INFORMATION:
APPLICANT: Knutson, Debbie
TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
FILE REFERENCE: WOCO.156.00US
CURRENT APPLICATION NUMBER: US/09/330,235
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: 60/089,043
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent Version 3.0
SEQ ID NO 3
LENGTH: 41
TYPE: DNA
ORGANISM: synthetic primer
US-09-330-235-3

Query Match 69.0%; Score 13.8; DB 3; Length 41;
Best Local Similarity 88.2%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGAGCCACGATGTC 17
DB 34 AATGAGCCACGATGTC 18

RESULT 8
US-09-396-196G-99591
Sequence 99591, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 99591
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-99591

Query Match 67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGCCACGAGTGTCCA 19
DB 11 AGCCACGAGTGTCCA 25

RESULT 9
US-09-396-196G-99592
Sequence 99592, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 99592
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-99592

Query Match 67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGCCACGAGTGTCCA 19
DB 5 AGCCACGAGTGTCCA 19

RESULT 10
US-09-396-196G-99593
Sequence 99593, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 99593
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-99593

Query Match 67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGCCACGAGTGTCCA 19
DB 2 AGCCACGAGTGTCCA 16

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RESULT 11
US-09-661-753-66/C
; Sequence 66, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0438
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-66

Query Match      66.0%; Score 13.2; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 ATGAGCCACCACTGTCCA 19
DB      19 ATGAGCTACTCTGGTCCA 2

RESULT 12
US-09-216-393B-208/C
; Sequence 208, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Mulhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDI PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 208
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-216-393B-208

Query Match      66.0%; Score 13.2; DB 3; Length 22;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 ATGAGCCACCACTGTCCA 19
DB      21 ATGATGACACCACTGTCCA 4

RESULT 13
US-09-396-196G-60900
; Sequence 60900, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
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FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60900
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60900

Query Match      66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 ATGAGCCACCACTGTCCA 19
DB      5 ATGAGCTACTCTGGTCCA 22

RESULT 14
US-09-396-196G-60901
; Sequence 60901, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60901
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60901

Query Match      66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 ATGAGCCACCACTGTCCA 19
DB      2 ATGAGCTACTCTGGTCCA 19

RESULT 15
US-10-131-827-6025/C
; Sequence 6025, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
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SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 6025
 ; LENGTH: 50
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-131-827-6025

Query Match 66.0%; Score 13.2; DB 3; Length 50;
 Best Local Similarity 83.3%; Pred. No. 2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 22 TGAACACCAAGTGTCCA 5

Search completed: May 21, 2006, 23:25:18
 Job time : 116.5 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: May 21, 2006, 22:09:18 ; Search time 654 Seconds
(without alignments)
375.769 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccacagtgccaa 20

Scoring table: IDENTITY NUC

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Searched: 18892170 seqs, 6143817638 residues 24111450

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US08_PUBCOMB.seq:*
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- 8: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10_PUBCOMB.seq:*
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- 12: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/pcodata/2/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	20	8 US-10-766-185-1	Sequence 1, Appl1
C 2	20	100.0	20	8 US-10-766-185-2	Sequence 2, Appl1
C 3	18.4	92.0	37	6 US-10-190-394-2	Sequence 187, Appl1
C 4	18	90.0	20	9 US-10-719-370A-187	Sequence 187, App
C 5	16.4	82.0	19	14 US-11-083-784-225584	Sequence 225584,
C 6	16.4	82.0	19	15 US-11-101-244-225584	Sequence 195175,
C 7	16	80.0	24	11 US-10-310-914A-185175	Sequence 515021,
C 8	15.8	79.0	25	9 US-10-719-900-515021	Sequence 650902,
C 9	15.8	79.0	25	15 US-11-121-849-650902	Sequence 334675,
C 10	15.4	77.0	25	8 US-10-719-956-334675	Sequence 571979,
C 11	15.4	77.0	25	9 US-10-719-900-571979	Sequence 650903,
C 12	15.2	76.0	25	15 US-11-121-849-650903	Sequence 655975,
C 13	15.2	76.0	25	15 US-11-121-849-655975	Sequence 124371,
C 14	14.8	74.0	19	14 US-11-083-784-124371	Sequence 124371,
C 15	14.8	74.0	19	14 US-11-101-244-124371	Sequence 243, App
C 16	14.8	74.0	20	13 US-11-039-629-243	Sequence 243, App
C 17	14.8	74.0	20	16 US-11-207-476-243	Sequence 243, App

C 18	14.8	74.0	25	8 US-10-719-956-517759	Sequence 517759,
C 19	14.8	74.0	25	9 US-10-719-900-289663	Sequence 289663,
C 20	14.8	74.0	25	9 US-10-719-900-417993	Sequence 417993,
C 21	14.8	74.0	25	9 US-10-719-900-852952	Sequence 852952,
C 22	14.8	74.0	25	13 US-11-036-317-724065	Sequence 724065,
C 23	14.8	74.0	43	9 US-10-783-557-428	Sequence 428, App
C 24	14.4	72.0	19	14 US-11-083-784-369850	Sequence 369850,
C 25	14.4	72.0	19	14 US-11-083-784-1242405	Sequence 1242405,
C 26	14.4	72.0	19	15 US-11-101-244-369850	Sequence 369850,
C 27	14.4	72.0	19	15 US-11-101-244-1242405	Sequence 1242405,
C 28	14.4	72.0	25	8 US-10-719-956-583062	Sequence 583062,
C 29	14.4	72.0	25	8 US-10-719-956-604657	Sequence 604657,
C 30	14.4	72.0	25	9 US-10-719-900-7136	Sequence 7136, Ap
C 31	14.4	72.0	25	9 US-10-719-900-299394	Sequence 299394,
C 32	14.4	72.0	25	9 US-10-719-900-589698	Sequence 589698,
C 33	14.4	72.0	25	13 US-11-036-317-195619	Sequence 195619,
C 34	14.4	72.0	25	13 US-11-036-317-228611	Sequence 228611,
C 35	14.4	72.0	25	13 US-11-036-317-23617	Sequence 23617,
C 36	14.4	72.0	25	13 US-11-036-317-268109	Sequence 268109,
C 37	14.4	72.0	25	13 US-11-036-317-314795	Sequence 314795,
C 38	14.4	72.0	25	13 US-11-036-317-358459	Sequence 358459,
C 39	14.4	72.0	25	13 US-11-036-317-578460	Sequence 578460,
C 40	14.4	72.0	25	13 US-11-060-756-134735	Sequence 134735,
C 41	14.4	72.0	25	15 US-11-121-849-412943	Sequence 412943,
C 42	14.2	71.0	21	10 US-10-847-918-65600	Sequence 65600, Ap
C 43	14.2	71.0	24	11 US-10-310-914A-28845	Sequence 28845, A
C 44	14.2	71.0	25	6 US-10-072-438-17	Sequence 17, Appl
C 45	14.2	71.0	25	6 US-10-137-765-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-10-766-185-1/c
; Sequence 1, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
; APPLICANT: Yoon, Heejeong
; APPLICANT: Ahn, Chang Ho
; APPLICANT: Lee, Young Bok
; APPLICANT: Mao, Lingjun
; APPLICANT: Jiang, Xiaoming
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
; FILE REFERENCE: REX 7034
; CURRENT APPLICATION NUMBER: US/10/766,185
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
US-10-766-185-1

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACAGTGCCAA 20
Db 20 AATGAGCCACAGTGCCAA 1

RESULT 2
US-10-766-185-2
; Sequence 2, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
; APPLICANT: Yoon, Heejeong
; APPLICANT: Ahn, Chang Ho
; APPLICANT: Lee, Young Bok
; APPLICANT: Mao, Lingjun

APPLICANT: Jiang, Xiaoming
TITLE OF INVENTION: Antisense oligonucleotides that inhibit expression of HIF-1
FILE REFERENCE: REX 7034
CURRENT APPLICATION NUMBER: US/10/766,185
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: antisense oligonucleotide
US-10-766-185-2

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACGAGTCCAA 20
DB 1 AATGAGCCACGAGTCCAA 20

RESULT 3
US-10-190-394-2
Sequence 2, Application US/10190394
Publication No. US20030018007A1
GENERAL INFORMATION:
APPLICANT: Gregory, Richard
APPLICANT: Vincent, Karen
TITLE OF INVENTION: Compositions and Methods for Inducing Gene
EXPRESSION
FILE REFERENCE: GA0112C1P2
CURRENT APPLICATION NUMBER: US/10/190,394
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US/09/579,897
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/067,546
PRIOR FILING DATE: 1997-12-04
PRIOR APPLICATION NUMBER: PCT/US98/25753
PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: 09/133,612
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 37
TYPE: DNA
ORGANISM: Homo sapiens
US-10-190-394-2

Query Match 92.0%; Score 18.4; DB 6; Length 37;
Best Local Similarity 95.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACGAGTCCAA 20
DB 8 AGTGAGCCACGAGTCCAA 27

RESULT 4
US-10-719-370A-187
Sequence 187, Application US/10719370A
Publication No. US2004020393A1
GENERAL INFORMATION:
APPLICANT: Ward, Donna T.
APPLICANT: Marchison, Eric G.
APPLICANT: Freiler, Susan W.
TITLE OF INVENTION: MODULATION OF HIF1A AND HIF2A EXPRESSION
FILE REFERENCE: ISPT-1010
CURRENT APPLICATION NUMBER: US/10/719,370A

CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US 10/304,126
PRIOR FILING DATE: 2002-11-23
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.2
SEQ ID NO 187
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-719-370A-187

Query Match 90.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGAGCCACGAGTCCAA 20
DB 1 TGAGCCACGAGTCCAA 18

RESULT 5
US-11-083-784-225584/C
Sequence 225584, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 225584
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-225584

Query Match 82.0%; Score 16.4; DB 14; Length 19;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACGAGTCC 18
DB 18 AGTGAGCCACGAGTCC 1

RESULT 6
US-11-101-244-225584/C
Sequence 225584, Application US/1101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/052,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 225584
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-225584

Query Match 82.0%; Score 16.4; DB 15; Length 19;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACGAGTCTCC 18
Db 18 AGTGAGCCACGAGTCTCC 1

RESULT 7
US-10-310-914A-195175
Sequence 195175, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087, 0200, CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patent in version 3.3
SEQ ID NO 195175
LENGTH: 24
TYPE: RNA
ORGANISM: Human
US-10-310-914A-195175

Query Match 80.0%; Score 16; DB 11; Length 24;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGCCACGAGTGTCCA 20
Db 1 AGCCACGAGTGTCCA 16

RESULT 8
US-10-719-900-515021/C
Sequence 515021, Application US/10719900
Publication No. US2005002616A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 515021
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-515021

Query Match 79.0%; Score 15.8; DB 9; Length 25;

Best Local Similarity 89.5%; Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AATGAGCCACGAGTCTCA 19
Db 21 AATGAGCCACGAGTCTCA 3

RESULT 9
US-11-121-849-650902/C
Sequence 650902, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 650902
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-650902

Query Match 79.0%; Score 15.8; DB 15; Length 25;
Best Local Similarity 89.5%; Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGAGCCACGAGTGTCCA 19
Db 23 AATGAGCCACGAGTGTCCA 5

RESULT 10
US-10-719-956-334675/C
Sequence 334675, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 334675
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-334675

Query Match 77.0%; Score 15.4; DB 8; Length 25;
Best Local Similarity 94.1%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACGAGTCTC 17
Db 17 AATGAGCCACGAGTCTC 1

RESULT 11
US-10-719-900-571979/C
Sequence 571979, Application US/10719900
Publication No. US2005002616A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou

;; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;; FILE REFERENCE: 3528.1
;; CURRENT APPLICATION NUMBER: US/10/719,900
;; CURRENT FILING DATE: 2003-11-20
;; PRIOR APPLICATION NUMBER: 60/427,808
;; PRIOR FILING DATE: 2002.11.20
;; NUMBER OF SEQ ID NOS: 982914
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 571979
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-10-719-900-571979

Query Match 77.0%; Score 15.4; DB 9; Length 25;
Best Local Similarity 94.1%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGAGCCACCACTGTCCA 19
DB 19 TGAGCCACCACTGTCCA 3

RESULT 12
US-11-121-849-650903/C
; Sequence 650903, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 650903
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-650903

Query Match 77.0%; Score 15.4; DB 15; Length 25;
Best Local Similarity 94.1%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCC 17
DB 18 AATGAGCCACCACTGTCC 2

RESULT 13
US-11-121-849-655975
; Sequence 655975, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 655975
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-655975

Query Match 76.0%; Score 15.2; DB 15; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCA 20
DB 1 AATGAGCCACCACTGTCCA 20

RESULT 14
US-11-083-784-1242371
; Sequence 1242371, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1242371
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1242371

Query Match 74.0%; Score 14.8; DB 14; Length 19;
Best Local Similarity 72.2%; Pred. No. 2.1e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGAGCCACCACTGTCCA 19
DB 2 AATGAGCCACCACTGTCCA 19

RESULT 15
US-11-101-244-1242371
; Sequence 1242371, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1242371
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1242371

US-11-101-244-1242371

Query Match 74.0%; Score 14.8; DB 15; Length 19;

Best Local Similarity 72.2%; Pred. No. 2.1e+03;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATGAGCCACCAAGTGTCCA 19

Db 2 AUGAGCCACCAUGUCUA 19

Search completed: May 21, 2006, 22:32:02
Job time : 656 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using bw model

Run on: May 21, 2006, 22:18:38 / Search time 32.5 Seconds
(without alignments)
43.419 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20
Sequence: 1 aatgagccaccagtgtccaa 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 307544

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA-New*

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- 3: /EMC_Celerra_SIDS3/prodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubpna/US08_NEW_PUB.seq:*
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- 8: /EMC_Celerra_SIDS3/prodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	25	US-11-217-529-13735	Sequence 13735, A
2	13.2	66.0	25	US-11-217-529-44186	Sequence 44186, A
3	13.2	66.0	25	US-11-217-529-86968	Sequence 86968, A
4	13.2	66.0	50	US-10-511-937-2733	Sequence 2733, Ap
5	13	65.0	25	US-11-217-529-74193	Sequence 74193, A
6	13	65.0	25	US-11-217-529-88752	Sequence 88752, A
7	12.8	64.0	25	US-11-217-529-9748	Sequence 9748, Ap
8	12.8	64.0	25	US-11-217-529-117069	Sequence 117069, A
9	12.6	63.0	25	US-11-217-529-22469	Sequence 22469, A
10	12.6	63.0	25	US-11-217-529-71644	Sequence 71644, A
11	12.6	63.0	25	US-11-217-529-125526	Sequence 125526, A
12	12.4	62.0	25	US-11-217-529-8089	Sequence 8089, Ap
13	12.4	62.0	25	US-11-217-529-45366	Sequence 45366, A
14	12.2	61.0	25	US-11-217-529-29471	Sequence 29471, A
15	12.2	61.0	25	US-11-217-529-38860	Sequence 38860, A
16	12.2	61.0	25	US-11-217-529-44089	Sequence 44089, A
17	12.2	61.0	25	US-11-217-529-89698	Sequence 89698, A
18	12.2	61.0	25	US-11-217-529-110177	Sequence 110177, A
19	12.2	61.0	25	US-11-217-529-132345	Sequence 132345, A
20	12.2	61.0	25	US-11-217-529-159967	Sequence 159967, A
21	12.2	61.0	26	US-11-257-502-110	Sequence 110, App
22	12	60.0	25	US-11-217-529-30855	Sequence 30855, A
23	12	60.0	25	US-11-217-529-38629	Sequence 38629, A
24	12	60.0	25	US-11-217-529-43480	Sequence 43480, A
25	12	60.0	25	US-11-217-529-56109	Sequence 56109, A

26	12	60.0	25	US-11-217-529-62922	Sequence 62922, A
27	12	60.0	25	US-11-217-529-90441	Sequence 90441, A
28	12	60.0	25	US-11-217-529-100966	Sequence 100966, A
29	12	60.0	25	US-11-217-529-133723	Sequence 133723, A
30	12	60.0	25	US-11-217-529-135675	Sequence 135675, A
31	12	60.0	25	US-11-217-529-155061	Sequence 155061, A
32	12	60.0	25	US-11-217-529-160487	Sequence 160487, A
33	12	60.0	25	US-11-217-529-166036	Sequence 166036, A
34	12	60.0	25	US-11-217-529-189912	Sequence 189912, A
35	12	60.0	25	US-11-217-529-189916	Sequence 189916, A
36	11.8	59.0	20	US-10-511-937-861	Sequence 861, App
37	11.8	59.0	25	US-11-217-529-25957	Sequence 25957, A
38	11.8	59.0	25	US-11-217-529-33050	Sequence 33050, A
39	11.8	59.0	25	US-11-217-529-34973	Sequence 34973, A
40	11.8	59.0	25	US-11-217-529-57598	Sequence 57598, A
41	11.8	59.0	25	US-11-217-529-64579	Sequence 64579, A
42	11.8	59.0	25	US-11-217-529-104375	Sequence 104375, A
43	11.8	59.0	25	US-11-217-529-141696	Sequence 141696, A
44	11.8	59.0	25	US-11-217-529-171657	Sequence 171657, A
45	11.6	58.0	25	US-11-217-529-6678	Sequence 6678, Ap

ALIGNMENTS

```

RESULT 1
US-11-217-529-13735/C
Sequence 13735, Application US/11217529
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIOHRO
APPLICANT: NAKAMURA, NORIHIISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIOHRO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13735
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-13735

Query Match      71.0% Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2% Pred. No. 21;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1 AATGAGCCACCGAGTGTCCA 19
Db      24 AATGAGCCACCGAGTGTCCA 6

RESULT 2
US-11-217-529-44186/C
Sequence 44186, Application US/11217529
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIOHRO
APPLICANT: NAKAMURA, NORIHIISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIOHRO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529

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CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 44186
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-44186

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATAGGCACCAAGTCTCC 18
22 AATGACCAACCAAGCTTC 5

RESULT 3

US-11-217-529-86968
Sequence 86968, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHITIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 86968
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-86968

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATAGGCACCAAGTCTCA 19
4 ATAGGCACCAAGTCTCA 21

RESULT 4

US-10-511-937-2733/C
Sequence 2733, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morille, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2733
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-2733

Query Match 66.0%; Score 13.2; DB 6; Length 50;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAGCCACCAAGTCTCA 20
22 TGAACCAACCAAGTCTCA 5

RESULT 5

US-11-217-529-74193/C
Sequence 74193, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHITIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 74193
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-74193

Query Match 65.0%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATAGGCACCAAGT 14
22 ATAGGCACCAAGT 10

RESULT 6

US-11-217-529-88752/C
Sequence 88752, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHITIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 88752
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-88752

Query Match
Best Local Similarity 65.0%; Score 13; DB 7; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGCCACCAG 13
Db 18 AATGAGCCACCAG 6

RESULT 7
US-11-217-529-9748
Sequence 9748, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 9748
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-9748

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGCCACCACTGTCCA 19
Db 7 GAGCCATCAGGCTCCA 22

RESULT 8
US-11-217-529-117069
Sequence 117069, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 117069
LENGTH: 25
TYPE: DNA

ORGANISM: Saccharomyces pastorianus
US-11-217-529-117069

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATGAGCCACCACTGTCTC 17
Db 6 ATGAGCCACCACTGTCTC 21

RESULT 9
US-11-217-529-22469
Sequence 22469, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 22469
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-22469

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATGAGCCACCACTGTCCA 20
Db 4 AAGAGCCACCTTGCCCA 22

RESULT 10
US-11-217-529-71644/c
Sequence 71644, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 71644
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-71644

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCA 19

Db 24 AATGAGCCACCACTGTCTACA 6

RESULT 11

US-11-217-529-125526
; Sequence 125526, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 125526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-125526

Query Match 63.0%; Score 12.6; DB 7; Length 25;

Best Local Similarity 78.9%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCA 19

Db 1 AATGAGCCACCACTGTGTACCA 19

RESULT 12

US-11-217-529-8089/c
; Sequence 8089, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8089
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-8089

Query Match 62.0%; Score 12.4; DB 7; Length 25;

Best Local Similarity 92.9%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGCCACCACTGTTC 17

Db 18 GAGCCACCACTGTTC 5

RESULT 13
US-11-217-529-45366
; Sequence 45366, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45366
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-45366

Query Match 62.0%; Score 12.4; DB 7; Length 25;

Best Local Similarity 92.9%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCACCACTGTCTCCA 20

Db 7 CCACCACTGTCTCCA 20

RESULT 14

US-11-217-529-29471/c
; Sequence 29471, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-29471

Query Match 61.0%; Score 12.2; DB 7; Length 25;

Best Local Similarity 82.4%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGCCACCACTGTCTCCA 20

Db 21 GAGCCACCACTCTCTCCA 5

RESULT 15

US-11-217-529-38860/c
; Sequence 38860, Application US/11217529


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; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIYO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38860
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-38860

```

```

Query Match      61.0%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      4 GAGCCACGAGTGTCCAA 20
      ||| ||||| |||
Db      21 GAGTACCGAGTGTACAA 5

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Search completed: May 21, 2006, 22:34:13
 Job time : 32.5 secs

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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:09:23 ; Search time 1331 Seconds
(without alignments)
960.893 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccggtgccaa 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_env:*
2: gb_pac:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
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10: gb_vl:*
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12: gb_hcg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 3	20	100.0	1252	5	HSTUNRA	X72726 H.sapiens t
C 4	20	100.0	3013	14	AY971808	AY971808 Pantholop
C 5	20	100.0	3217	6	DQ229099	DQ229099 Bos palax
C 6	20	100.0	3296	14	AY621118	AY621118 Bos grum
C 7	20	100.0	3669	5	AB169332	AB169332 Macaca fa
C 8	20	100.0	188107	5	CNS01DME	AL137129 Human chr
C 9	20	100.0	248982	12	AC156150	AC156150 Bos tauru
C 10	18.4	92.0	311	2	AX986444	AX986444 Sequence
C 11	18.4	92.0	311	2	BD121303	BD121303 EST and e
C 12	18.4	92.0	311	2	AR425750	AR425750 Sequence
C 13	18.4	92.0	375	2	C0696751	C0696751 Sequence
C 14	18.4	92.0	1172	7	G26793	G26793 human STS S
C 15	18.4	92.0	1558	5	HSHIF1A13	AF050127 Homo sapi
C 16	18.4	92.0	2537	5	AF207602	AF207602 Homo sapi
C 17	18.4	92.0	2711	6	RNHYPAC1	Y09507 R.norvegicu
C 18	18.4	92.0	3229	2	ARS31606	ARS31606 Sequence

C 19	18.4	92.0	3551	5	AB073325	AB073325 Homo sapi
C 20	18.4	92.0	3678	2	AR367892	AR367892 Sequence
C 21	18.4	92.0	3678	2	AR642314	AR642314 Sequence
C 22	18.4	92.0	3678	2	AX504300	AX504300 Sequence
C 23	18.4	92.0	3678	2	AX770508	AX770508 Sequence
C 24	18.4	92.0	3678	5	HSU22431	U22431 Human hypox
C 25	18.4	92.0	3736	2	BD222980	BD222980 Stable hy
C 26	18.4	92.0	3736	2	AR317244	AR317244 Sequence
C 27	18.4	92.0	3913	2	C0719027	C0719027 Sequence
C 28	18.4	92.0	3927	2	AX321214	AX321214 Sequence
C 29	18.4	92.0	3933	2	AX763546	AX763546 Sequence
C 30	18.4	92.0	3933	5	BC012527	BC012527 Homo sapi
C 31	18.4	92.0	3933	5	HSU29165	U29165 Human MOP1
C 32	18.4	92.0	3945	5	HSMB08946	BS648795 Homo sapi
C 33	18.4	92.0	3958	2	CS097358	CS097358 Sequence
C 34	18.4	92.0	231045	12	AC118105	AC118105 Rattus no
C 35	18.4	92.0	284456	12	AC174572	AC174572 Bos tauru
C 36	18.4	92.0	298281	12	AC174569	AC174569 Bos tauru
C 37	18.4	90.0	450	7	BV003723	BV003723 S208P467
C 38	18.4	90.0	1321	6	AF006789S15	AF006789 Mus muscu
C 39	18.4	90.0	3392	6	DQ010149	DQ010149 Microtus
C 40	18.4	90.0	3718	2	AX694334	AX694334 Sequence
C 41	18.4	90.0	3718	6	AF057308	AF057308 Rattus no
C 42	18.4	90.0	3746	2	AX306008	AX306008 Sequence
C 43	18.4	90.0	3746	6	MHIF1ALP	X95580 M.musculus
C 44	18.4	90.0	3867	6	MMU59496	U59496 Mus musculu
C 45	18.4	90.0	3973	6	AF003695	AF003695 Mus muscu

ALIGNMENTS

RESULT 1
G72559/c 492 bp DNA linear STS 08-AUG-2001
DEFINITION MARC 6691-6694:992007331.1 SCF - porcine spleen Sus scrofa STS
ACCESSION G72559 genomic, sequence tagged site.
VERSION G72559.1 GI:15146589
KEYWORDS STS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae; Sus 1 (bases 1 to 492)
Fahnenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L. and Keeler,J.W.
Single nucleotide polymorphism (SNP) discovery in expressed porcine genes
Unpublished (2001)

JOURNAL COMMENT

Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4276
Fax: 402 762 4173
Email: freking@ma.ars.usda.gov
Primer A: TACGAGCAGCAGAACCTAC
Primer B: TGTGCAATGTGCTACTC
STS size: 520
PCR Profile:
Hotstart: 95 degrees for 15 minutes
Denature: 95 degrees for 30 seconds
Anneal: 58 degrees
Extension: 68 degrees for 2 minutes
Cycles: 32 to 45
Protocol:
Template: 50-200 ng genomic DNA
Primer: each 20 pmol
dNTPs: each 88 uM
Tag Polymerase: 0.25 units (Qiagen HotStar)

Buffer:
Commercially supplied Qiagen HotStar buffer

The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater. Amplicon size was estimated by agarose gel electrophoresis.

FEATURES

source

Location/Qualifiers

1..492
/organism="Sus scrofa"
/mol_type="genomic DNA"
/strain="white composite, duroc, meishan, minzhu, fengjing, crossbreds"
/db_xref="taxon:9823"
/sex="male and female"
/clone_lib="SCF - porcine spleen"
/dev_stage="adult"
/note="Organ: spleen"
<1..>492

ORIGIN

STS

Query Match 100.0%; Score 20; DB 7; Length 492;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACGAGTGTCCAA 20
|||||
94 AATGAGCCACGAGTGTCCAA 75

RESULT 2

G72558/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

G72558 928 bp DNA linear STS 08-AUG-2001
DEFINITION MARC 6693-6692:992007336.1 SCF - porcine spleen Sus scrofa STS
ACCESSION G72558
VERSION G72558.1 GI:15146588
KEYWORDS STS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE 1 (bases 1 to 928)
AUTHORS Fahnenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L. and Keefe,J.W.
TITLE Single nucleotide polymorphism (SNP) discovery in expressed porcine genes
JOURNAL Unpublished (2001)

Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
Email: freking@ma.ars.usda.gov
Primer A: TGTGAGTTATGCTCTATA
Primer B: AAAAGAGTTTATATAGGAC
STS size: 560
PCR Profile:

Hotstart: 95 degrees for 15 minutes
Denature: 95 degrees for 30 seconds
Anneal: 58 degrees
Extension: 68 degrees for 2 minutes
Cycles: 32 to 45
Protocol:

Template: 50-200 ng genomic DNA
Primer: each 20 pmols
dNTPs: each 88 uM

Tag Polymerase: 0.25 units (Qiagen HotStar)

Buffer:
Commercially supplied Qiagen HotStar buffer

The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater. Amplicon size was estimated by agarose gel electrophoresis.

FEATURES

source

Location/Qualifiers

1..928
/organism="Sus scrofa"
/mol_type="genomic DNA"
/strain="white composite, duroc, meishan, minzhu, fengjing, crossbreds"
/db_xref="taxon:9823"
/sex="male and female"
/clone_lib="SCF - porcine spleen"
/dev_stage="adult"
/note="Organ: spleen"
<1..>928

ORIGIN

STS

Query Match 100.0%; Score 20; DB 7; Length 928;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACGAGTGTCCAA 20
|||||
57 AATGAGCCACGAGTGTCCAA 38

RESULT 3

HSTNPA/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

source

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

Location/Qualifiers

1..1252
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="9"
/clone="KL, A"
/cell_line="AMA cells"

HSTNPA 1252 bp mRNA linear PRI 27-OCT-1995
DEFINITION H.sapiens tump mRNA for transformation upregulated nuclear protein, exon D.
ACCESSION X72726
VERSION X72726.1 GI:460774
KEYWORDS transformation upregulated nuclear protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1252)
AUTHORS Dejgaard,K., Leffers,H., Rasmussen,H.H., Madsen,P., Kruse,T.A., Gesser,B., Nielsen,H. and Celis,J.E.
TITLE Identification, molecular cloning, expression and chromosome mapping of a family of transformation upregulated hURP-K proteins derived by alternative splicing
J. Mol. Biol. 236 (1), 33-48 (1994)
810714
2 (bases 1 to 1252)
Leffers,H.
DIRECT SUBMISSION
Submitted (18-MAR-1993) H. Leffers, Institute of Medical Biochemistry and Danish Centre for Human Genome Research, Ole Worms Alle 170, Aarhus University, 8000 Aarhus, DENMARK
Alternatively spliced exon A, B, C - see X72727
Overlaps with U22431.

polya_signal /clone_1lb="lambda ZAP II cDNA"
ORIGIN 1229. .1234

Query Match 100.0%; Score 20; DB 5; Length 1252;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCA 20
|||||
Db 126 AATGAGCCACCAAGTGTCCA 107

RESULT 4
AY971808/c 3013 bp mRNA linear MAM 20-APR-2005
LOCUS Pantholops hodgsoni hypoxia inducible factor-1 alpha mRNA,
DEFINITION complete cds.
ACCESSION AY971808
VERSION AY971808.1 GI:62632234
KEYWORDS
SOURCE
ORGANISM Pantholops hodgsoni (chiru)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Artiodactyla; Pantholops.
REFERENCE
AUTHORS 1 (bases 1 to 3013)
Xie,Z.-Y., Chen,X.-Q., Du,J.-Z., Li,H.-Q., Wang,T.-Y. and
Xiao,P.-H.
TITLE Cloning of HIF-1 alpha cDNA from Tibetan antelope (Pantholops
hodgsoni)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3013)
Xie,Z.-Y., Chen,X.-Q., Du,J.-Z., Li,H.-Q., Wang,T.-Y. and
Xiao,P.-H.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2005) Department of Biotechnology, College of
Life Sciences, Room 229, Teaching Building Eight, Yunnan Campus,
Zhejiang University and Qinghai Kekexili National Nature Reserve,
Hangzhou, Zhejiang 310027, PR China
FEATURES
source
Location/Qualifiers
1..3013
/organism="Pantholops hodgsoni"
/mol_type="mRNA"
/db_xref="taxon:59538"
/cissue_type="muscle"
32..2503
/codon_start=1
/product="hypoxia inducible factor-1 alpha"
/protein_id="AAH89137.1"
/db_xref="GI:62632234"
/translation="MEGAGAGDADKKISERKESRDPAARRSRKESSEVYELAHQ
LPLPNVSHLDKASVMRLTISYLVRKLLDGDLDIEDMAQNNCFYLKALDGVN
LTDGDMIVISDNVKNMGLTFELTGHSDVDFTHPCDHEKREMLTRNGVADGKE
ONTQSPFLPMKCTLSRGRTNIIKSAITKALHGTGHIHYDTNSNOCGCKKPM
CIVLCBPIPHPSNIEIPLDSTKPLSRSLDKMFSYCDERITELMGVEBELGSIY
EYVHALSDHLTKTHDMFTKQVLTQYRLARGGVWVETATVITNTKNSQPQ
IVCVNVVSGIIGHDLIFSLQTECVKPVSSDMKMTQLFTKESBDTSI.FDILK
EEDATLTLAPAGDTIISLDGSDTEDEDDQLSDVPLXNVMFPSSDDKLSINLA
SPLPASPKEPKRENADPALNOEVALKLEPAASLEISFTMPOIODOPASPDGSTR
SSPBNPSEYCPVDSDMNVFGLVETKPADTRAKNPFSTDDTDLMLAPY
PMDDPOLRSFQSLPLESSPNPVSVAFOQTOLQEPITITTTTBSLKVTKOST
EDIKLITSPSTHTPKETTTATYSSPYSGTQSRFASPVRAQGVLEQEKSHPRPN
VLSTVLSQRTNVBEELNPKIILQNAQRKRMEDGSLFOAGIGTLIQCPDDRAPA
TSLSKRVKSGSGONMEQKTIILIPSDLACRLGQSMDSGLPOLTSYCEVNA
VVAPIQGSRLNLOGBELRALDQVN"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 3013;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCA 20

|||||
Db 2549 AATGAGCCACCAAGTGTCCA 2530

RESULT 5
DQ229099/c 3217 bp mRNA linear ROD 29-OCT-2005
LOCUS Bospalax baileyi hypoxia inducible factor 1 alpha subunit mRNA,
DEFINITION complete cds.
ACCESSION DQ229099
VERSION DQ229099.1 GI:78058355
KEYWORDS
SOURCE
ORGANISM Bospalax baileyi
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Spalacidae; Myospalacinae; Bospalax.
REFERENCE
AUTHORS 1 (bases 1 to 3217)
Chen,X.-Q., Xie,Z.-Y. and Du,J.-Z.
TITLE Cloning of hypoxia-inducible factor 1 alpha from plateau zokor
(Myospalax baileyi)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3217)
Chen,X.-Q., Xie,Z.-Y. and Du,J.-Z.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology,
Zhejiang University, Zheda Road 38#, Teaching Building 8, Room 229,
Yunnan Campus, Hangzhou, Zhejiang 310027, China
FEATURES
source
Location/Qualifiers
1..3217
/organism="Bospalax baileyi"
/mol_type="mRNA"
/db_xref="taxon:146132"
/cissue_type="liver"
17..2476
/note="HIF-1alpha"
/codon_start=1
/product="hypoxia inducible factor 1 alpha subunit"
/protein_id="BAB17537.1"
/db_xref="GI:78058356"
/translation="MEGAGAGGEEKNNRMSSEKRSRDAARRSRKESSEVYELAHQ
LPLPNVSHLDKASVMRLTISYLVRKLLDGDLDIEDMAQNNCFYLKALDGVN
LTDGDMIVISDNVKNMGLTFELTGHSDVDFTHPCDHEKREMLTRNGVADGKE
EONTQSPFLPMKCTLSRGRTNIIKSAITKALHGTGHIHYDTNSNOCGCKKPM
TCVLCBPIPHPSNIEIPLDSTKPLSRSLDKMFSYCDERITELMGVEBELGSIY
EYVHALSDHLTKTHDMFTKQVLTQYRLARGGVWVETATVITNTKNSQPQ
CIVCVNVVSGIIGHDLIFSLQTECVKPVSSDMKMTQLFTKESBDTSI.FDILK
KSPDALTLAPAGDTIISLDGSDTEDEDDQLSDVPLXNVMFPSSDDKLSINLA
MSPLPASPKEPKRENADPALNOEVALKLEPAASLEISFTMPOIODOPASPDGSTR
OSSPBNPSEYCPVDSDMNVFGLVETKPADTRAKNPFSTDDTDLMLAPY
PMDDPOLRSFQSLPLESSPNPVSVAFOQTOLQEPITITTTTBSLKVTKOST
EDIKLITSPSTHTPKETTTATYSSPYSGTQSRFASPVRAQGVLEQEKSHPRPN
VLSTVLSQRTNVBEELNPKIILQNAQRKRMEDGSLFOAGIGTLIQCPDDRAPA
TSLSKRVKSGSGONMEQKTIILIPSDLACRLGQSMDSGLPOLTSYCEVNA
VVAPIQGSRLNLOGBELRALDQVN"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3217;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCA 20
|||||
Db 2581 AATGAGCCACCAAGTGTCCA 2562

RESULT 6

AY621118/c 3296 bp mRNA linear MAM 07-JUN-2004
LOCUS Bos grunniens hypoxia inducible factor-1a (HIF-1A) mRNA, complete
DEFINITION cds.
ACCESSION AY621118
VERSION AY621118.1 GI:47933908

KEYWORDS
SOURCE
ORGANISM

Bos grunniens (domestic yak)
Bos grunniens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bovinae; Bos.
1 (bases 1 to 3296)
Dolt, K.S. and Qader Pasha, M.A.
Direct Submission
Submitted (10-MAY-2004) Functional Genomics Unit, Institute of
Genomics and Integrative Biology, Mall Road, Delhi 110007, India

FEATURES
source
1..3296
/organism="Bos grunniens"
/mol_type="RNA"
/db_xref="taxon:30521"
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2..2473
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/note="bHLH transcription factor"
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/translation="MEGAGAGANDKKKISSERRKESRDAAASRSKSEFVYELAHOL
PLPHNVSSHLDKASVRLITSLVRKALDAGDDIDEDMAQKPCFYALKALDFVW
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QNTORSEFLRMKCTLTSGRTWIKSATWIKLHCTGHIVYDINSQSCGKPKPMT
CIVLICEPIPHSNIETPLDSTKFLSRHSLDMKFSYCDERITELMGEYELGSRIT
EYHALDSHILTKTHHGMFTKGYTTOGYRLAKRGVYVWVETQATVYNTNSQPC
IYCVNVVSGIIOHDLFSLQTECVLKPVESDMKQWOLFVYVSEDPISLFDIKK
EPDALULAPAAAGDTTISDRGSDTETDQCEEPYLVNDVLPESNRKQNTINLAK
SPLPNSERKPLSSADPALNDVALKLPNPESLSTPMQIQQPSFSDGSTRQ
SSPEPSPSEPCFSDVDNVEKELVSKLPADTEAKNPSTQTDIDLEMLAVI
PMDDDPOLRSPOLSPLENSSTSPQASTVTVPYQMOEPIATVTTATDELEKPI
TQGMEDIKILAFSPHPVPEKPCATSTPSDTSRTASPRAGKVIETDEKHP
RSPNVLSVALSRTDIAPEERINPLALQNAOKRKIEHDSGLFOGVGICLLQOPD
RATTSLSKRYKCKSSSQNGEQITLILPSDLACRLGQSDSGLPQLTSDICE
VNAPIQGSNHLQGEELRALDQVN"
2474..3296
/gene="HIF-1A"

ORIGIN
3'UTR

Query Match 100.0%; Score 20; DB 14; Length 3296;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACAGTGTCCAA 20
|||||
DB 2519 AATGAGCCACAGTGTCCAA 2500

RESULT 7
ABI69332/c
LOCUS
DEFINITION

ABI69332 3669 bp mRNA linear pri 17-SEP-2005
Macaca fascicularis testis cDNA, clone: Qcsa-19088, similar to
human hypoxia-inducible factor 1, alpha subunit
(basic helix-loop-helix transcription factor) (HIF1A), transcript
variant 1, mRNA, RefSeq: NM_001530.2.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

ABI69332
ABI69332.1 GI:67970145
oligo capping; f1a (full insert sequence).
Macaca fascicularis (craab-eating macaque)
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.
1
Osada, N., Hirata, M., Tanuma, R., Kusuda, J., Hida, M., Suzuki, Y.,
Sugano, S., Gotohori, T., Shen, C.-K.J., Wu, C.J. and Hashimoto, K.
Substitution Rate and Structural Divergence of 5'UTR Evolution:
Comparative Analysis Between Human and Cynomolgus Monkey cDNAs

JOURNAL
PUBMED
REFERENCE
AUTHORS
CONSTRM
TITLE

MoL. Biol. Evol. 22 (10), 1976-1992 (2005)
15944441
2
International consortium for macaque cDNA sequencing and analysis
DNA sequences of macaque genes expressed in brain or testis and its
evolutionary implications
Unpublished
3 (bases 1 to 3669)
Hashimoto, K., Kusuda, J. and Sugano, S.
Direct Submission
Submitted (18-MAR-2004) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources, 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)
The international consortium for macaque cDNA sequencing and
analysis consists of: Department of Virology and Human Genome
Center, Institute of Medical Science, The University of Tokyo,
Tokyo, Japan; Division of Genetic Resources, National Institute of
Infectious Diseases of Japan, Tokyo, Japan; National Health
Research Institute, Taipei, Taiwan; Institute of Molecular Biology,
Academia Sinica, Taipei, Taiwan; Department of Ecology & Evolution,
University of Chicago, Chicago, IL, USA; Center for Information
Biology, National Institute of Genetics of Japan, Mishima, Japan.
Clone distribution: clone distribution information can be found at:
http://www.nih.go.jp/yoken/genebank/
lab host: TOP10
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: DraIII (CACTGTCG)
R. Site2: DraIII (CAGCAGTCG)
Description: 1st strand cDNA was primed with an oligo(dT) primer
(ATGCGCTTTTCTTTTCTTTT), double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
the DraIII sites can be used to isolate the cDNA insert. Libraries
were constructed by oligo-capping method. Libraries were made from:
Qcde: cerebellum cortex
Qnpa: parietal lobe
Qtra: temporal lobe right
Qfla: frontal lobe left
Qma: medulla oblongata
Qbsa: brain stem
Qora: occipital lobe right
Qcsa: testis
Custom primers were used for 5' and 3'-end sequencing. The
full-insert sequencing was done by primer-walking method using ABI
DNA sequencer.
Location/Qualifiers
1..3669
/organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xref="taxon:9541"
/clone="Qcsa-19088"
/sex="male"
/clone_lib="macaque cDNA library Qcsa"
/dev_stage="adult"
297..2777
/note="unlabeled protein product; Homo sapiens
hypoxia-inducible factor 1, alpha subunit
(basic helix-loop-helix transcription factor)
(HIF1A), transcript variant 1, mRNA, RefSeq: NM_001530.2"
/codon_start=1
/protein_id="BAB01417.1"
/db_xref="GI:67970145"
/translation="MEGAGAGANDKKKISSERRKESRDAAASRSKSEFVYELAHOL
PLPHNVSSHLDKASVRLITSLVRKALDAGDDIDEDMAQKPCFYALKALDFVW
LTDGDMITISDVNKTGLTQFELTGHVSFDPFPCDEKEMKLTNRNGLVKQKE
QNTORSEFLRMKCTLTSGRTWIKSATWIKLHCTGHIVYDINSQSCGKPKPMT
CIVLICEPIPHSNIETPLDSTKFLSRHSLDMKFSYCDERITELMGEYELGSRIT
EYHALDSHILTKTHHGMFTKGYTTOGYRLAKRGVYVWVETQATVYNTNSQPC

gap 164002..164051
/estimated_length=50
gap 226342..226391
/estimated_length=50
gap 230590..230639
/estimated_length=50
gap 235990..236089
/estimated_length=unknown
gap 242227..242276
/estimated_length=50
gap 244359..244458
/estimated_length=unknown
gap 245461..245560
/estimated_length=unknown
gap 246565..246664
/estimated_length=unknown
gap 247680..247779
/estimated_length=unknown
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 18.4; DB 2; Length 248982;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
Db 187060 AATGAGCCACCAAGTGTCCAA 187079

RESULT 10
LOCUS AX986444 311 bp DNA linear PAT 15-JAN-2004
DEFINITION Sequence 17247 from Patent EP1104808.
ACCESSION AX986444
VERSION AX986444.1 GI:40992584
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1
Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
ESTs and encoded human proteins
Patent: EP 1104808-A 17247 06-JUN-2001;
Genet (FR)

FEATURES
source Location/Qualifiers
1..311
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 92.0%; Score 18.4; DB 2; Length 311;
Best Local Similarity 95.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
Db 198 AGTGAAGCCACCAAGTGTCCAA 179

RESULT 11
BD121303/c 311 bp DNA linear PAT 18-SEP-2002
LOCUS BD121303
DEFINITION EST and encoded human protein.
ACCESSION BD121303
VERSION BD121303.1 GI:23216213
KEYWORDS JP 2002010789-A/13380.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.
1 (bases 1 to 311)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 13380 15-JAN-2002;
GENSET CORP

COMMENT
OS Homo sapiens (human)
PN JP 2002010789-A/13380
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein
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location/Qualifiers
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Best Local Similarity 95.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
Db 198 AGTGAAGCCACCAAGTGTCCAA 179

RESULT 12
AR425750/c 311 bp DNA linear PAT 18-DEC-2003
LOCUS AR425750
DEFINITION Sequence 17247 from patent US 6639063.
ACCESSION AR425750
VERSION AR425750.1 GI:40180860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 311)
Edwards, J.B.D.M., Jobert, S. and Giordano, J.Y.
EST's and encoded human proteins
Patent: US 6639063-A 17247 28-OCT-2003;
Genet S.A.;

FEATURES
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Best Local Similarity 95.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
Db 198 AGTGAAGCCACCAAGTGTCCAA 179

RESULT 13
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LOCUS C0696751
DEFINITION Sequence 41677 from Patent WO02070737.
ACCESSION C0696751

VERSION C0696751.1 GI:42246561
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Liew, C.C., Marshall, W.B. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 0207037-A 41677 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 95.0%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATGAGCCACCACTGTCCAA 20
165 AGTGAGCCACCACTGTCCAA 146
Db
RESULT 14
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LOCUS human STS_U22431, sequence tagged site.
DEFINITION G26793
ACCESSION G26793.1 GI:1349025
VERSION STS; STS sequence; primer; sequence tagged site.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Hudson, T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
JOURNAL Mapped STS
COMMENT Unpublished (1995)
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu
Primer A: TGAACACTGTGCTCACTA
Primer B: ATGCTACTGCATGCAATG
STS size: 223
PCR Profile:
Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul
Buffer:
MgCl2: 1.5 mM

KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3
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location/Qualifiers
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Query Match 92.0%; Score 18.4; DB 7; Length 1172;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATGAGCCACCACTGTCCAA 20
49 AGTGAGCCACCACTGTCCAA 30
Db
RESULT 15
HSRIF1A13/c 1558 bp DNA linear PRI 26-OCT-1998
LOCUS Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) gene,
DEFINITION exon 15 and complete cds.
ACCESSION AF050127
VERSION AF050127.1 GI:3790533
KEYWORDS 13 of 13
SEGMENT Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Iyer, N.V., Leung, S.W. and Semenza, G.L.
TITLE The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
JOURNAL evolutionary conservation
PUBMED Genomics 52 (2), 159-165 (1998)
9782081
2 (bases 1 to 1558)
REFERENCES Iyer, N.V., Leung, S.W. and Semenza, G.L.
AUTHORS Direct Submission
JOURNAL Submitted (24-FEB-1998) Department of Pediatrics and Medicine,
Institute of Genetic Medicine, Johns Hopkins University School of
Medicine, 600 N. Wolfe St, Baltimore, MD 21287-3914, USA
FEATURES
source location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="14"
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AF050123..1:1..527,AF050124..1:1..996,AF050125..1:1..551,
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AF050124..1:120..406,AF050125..1:219..341,
AF050126..1:1469..902,AF050127..1:184..292,
AF050128..1:138..264,93..1413)
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CDS

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AF050121.1:134..281,AF050122.1:188..408,
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QNTORSFPLAMKCTLTSRGRTNINKSATWYLTGTHIHVDTNSNOQGVKKRPWT
CLYLICERPIHPSPNIEIPLDKRTPLSRHSIDMKFSYCDERITELMGTEPEELGRSII
EYHALDSDLTKTHDMFTKQVTTQYRLARQGVWVEVTOATVINYTKNSQPOC
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/number=14

93..1413

/gene="HIF1A"

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1395..1400

/gene="HIF1A"

IntIntron

3'UTR

polyA_signal

ORIGIN

Query Match

Best Local Similarity 92.0%; Score 18.4; DB 5; Length 1558;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACAGTCCAA 20

DB 290 AGTGGCCACAGTCCAA 271

Search completed: May 21, 2006, 22:18:19
Job time: 1334 secs

CC The invention describes a compound, RX-0047 or RX-0149 targeted to a
CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
CC where the oligonucleotide compound inhibits the expression of human HIF-
CC 1. Also described are: a method of inhibiting the expression HIF-1 in
CC human cells or tissues; and a method of inducing cytotoxicity in a cancer
CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a
CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'
CC aatgagccaccagctccaa 3' and SEQ ID NO. 4, 5' ggagctacatctccaagtc 3',
CC respectively). The compounds are useful for inhibiting the expression of
CC HIF-1 and inducing the cytotoxicity in several cancer cells. The
CC antisense compounds are also useful for preventing or delaying infection,
CC inflammation, or tumour formation. This sequence represents a human HIF-1
CC antisense oligonucleotide.

XX
SQ Sequence 20 BP, 7 A, 6 C, 4 G, 3 T, 0 U, 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTCCAA 20
DB 1 AATGAGCCACCAGTCCAA 20

RESULT 2

AD088721/c
ID AD088721 standard; DNA, 20 BP.

AC AD088721;

DT 21-OCT-2004 (first entry)

DE Human hypoxia inducible factor-1 gene fragment seqid 1.

XX RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;
KM cancer; infection; inflammation; tumour formation; ss.

XX Homo sapiens.

XX US2004152655-A1.

PD 05-AUG-2004.

XX 28-JAN-2004; 2004US-00766185.

PR 31-JAN-2003; 2003US-044367P.

XX (YOON/) YOON H.

PA (MAOL/) MAO L.

PA (LEBY/) LEE Y B.

PA (AHNC/) AHN C.

PA (JIAN/) JIANG X.

PI Yoon H, Mao L, Lee YB, Ahn C, Jiang X;

XX WPI; 2004-561492/54.

DR New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a
XX nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
XX useful for inhibiting expression of HIF-1 and inducing cytotoxicity in
XX several cancer cells.

PS Disclosure; SEQ ID NO 1, 35pp; English.

XX The invention describes a compound, RX-0047 or RX-0149 targeted to a
CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
CC where the oligonucleotide compound inhibits the expression of human HIF-
CC 1. Also described are: a method of inhibiting the expression HIF-1 in
CC human cells or tissues; and a method of inducing cytotoxicity in a cancer
CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a
CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'
CC aatgagccaccagctccaa 3' and SEQ ID NO. 4, 5' ggagctacatctccaagtc 3',

CC respectively). The compounds are useful for inhibiting the expression of
CC HIF-1 and inducing the cytotoxicity in several cancer cells. The
CC antisense compounds are also useful for preventing or delaying infection,
CC inflammation, or tumour formation. This sequence represents a site on the
CC HIF-1 to which antisense oligonucleotides can be targeted in order to
CC control HIF-1 gene expression.

XX
SQ Sequence 20 BP, 3 A, 4 C, 6 G, 7 T, 0 U, 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 20 AATGAGCCACCAGTCCAA 1

RESULT 3

AAK77781
ID AAK77781 standard; DNA, 27884 BP.

AC AAK77781;

DT 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32593.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

XX WO200157182-A2.

PD 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205151P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216477P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225470P.

PR 14-AUG-2000; 2000US-0225477P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226281P.

PR 22-AUG-2000; 2000US-0226288P.

PR 22-AUG-2000; 2000US-0227182P.

PR	23-AUG-2000	2000US-0227009P	PR	17-NOV-2000	2000US-0249210P
PR	30-AUG-2000	2000US-0228924P	PR	17-NOV-2000	2000US-0249211P
PR	01-SEP-2000	2000US-0229287P	PR	17-NOV-2000	2000US-0249212P
PR	01-SEP-2000	2000US-0229343P	PR	17-NOV-2000	2000US-0249213P
PR	01-SEP-2000	2000US-0229344P	PR	17-NOV-2000	2000US-0249214P
PR	01-SEP-2000	2000US-0229345P	PR	17-NOV-2000	2000US-0249215P
PR	05-SEP-2000	2000US-0229559P	PR	17-NOV-2000	2000US-0249216P
PR	05-SEP-2000	2000US-0229551P	PR	17-NOV-2000	2000US-0249217P
PR	06-SEP-2000	2000US-0230437P	PR	17-NOV-2000	2000US-0249218P
PR	06-SEP-2000	2000US-0231242P	PR	17-NOV-2000	2000US-0249244P
PR	08-SEP-2000	2000US-0231243P	PR	17-NOV-2000	2000US-0249245P
PR	08-SEP-2000	2000US-0231244P	PR	17-NOV-2000	2000US-0249246P
PR	08-SEP-2000	2000US-0231413P	PR	17-NOV-2000	2000US-0249265P
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PR	08-SEP-2000	2000US-0232080P	PR	17-NOV-2000	2000US-0249297P
PR	12-SEP-2000	2000US-0231968P	PR	17-NOV-2000	2000US-0249299P
PR	14-SEP-2000	2000US-0232337P	PR	17-NOV-2000	2000US-0249300P
PR	14-SEP-2000	2000US-0232338P	PR	01-DEC-2000	2000US-0250160P
PR	14-SEP-2000	2000US-0232339P	PR	01-DEC-2000	2000US-0250391P
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PR	14-SEP-2000	2000US-0233063P	PR	06-DEC-2000	2000US-0256719P
PR	14-SEP-2000	2000US-0233064P	PR	08-DEC-2000	2000US-0251479P
PR	21-SEP-2000	2000US-0233065P	PR	08-DEC-2000	2000US-0251856P
PR	21-SEP-2000	2000US-0234223P	PR	08-DEC-2000	2000US-0251868P
PR	21-SEP-2000	2000US-0234274P	PR	08-DEC-2000	2000US-0251869P
PR	25-SEP-2000	2000US-0234997P	PR	08-DEC-2000	2000US-0251989P
PR	25-SEP-2000	2000US-0234998P	PR	11-DEC-2000	2000US-0251990P
PR	26-SEP-2000	2000US-0235484P	PR	05-JAN-2001	2000US-0254097P
PR	27-SEP-2000	2000US-0235834P	XX	(HUMA-) HUMAN GENOME SCI INC.	
PR	27-SEP-2000	2000US-0235836P	XX	Rosen CA, Barash SC, Ruben SM,	
PR	29-SEP-2000	2000US-0236327P	XX	WPI; 2001-483426/52.	
PR	29-SEP-2000	2000US-0236367P	DR		
PR	29-SEP-2000	2000US-0236368P	XX		
PR	29-SEP-2000	2000US-0236369P	XX		
PR	29-SEP-2000	2000US-0236370P	PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PR	02-OCT-2000	2000US-0236802P	XX	useful for preventing, diagnosing and/or treating cancers and metastasis.	
PR	02-OCT-2000	2000US-0237037P	XX		
PR	02-OCT-2000	2000US-0237038P	PS	Disclosure; SEQ ID NO 32593; 3071bp + Sequence Listing; English.	
PR	02-OCT-2000	2000US-0237039P	XX		
PR	02-OCT-2000	2000US-0237040P	XX		
PR	13-OCT-2000	2000US-0239335P	CC	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)	
PR	13-OCT-2000	2000US-0239337P	CC	amino acid sequences given in AAK62170 to AAK61921. (I) have cytosolic	
PR	20-OCT-2000	2000US-0240960P	CC	activity, and can be used in gene therapy and vaccine production. (I)	
PR	20-OCT-2000	2000US-0241212P	CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
PR	20-OCT-2000	2000US-0241856P	CC	treatment of diseases associated with inappropriate (I) expression. For	
PR	20-OCT-2000	2000US-0241857P	CC	example, they may be used to treat disorders associated with decreased	
PR	20-OCT-2000	2000US-0241786P	CC	expression by rectifying mutations or deletions in a patient's genome	
PR	20-OCT-2000	2000US-0241808P	CC	that affect the activity of (I) by expressing inactive proteins or to	
PR	20-OCT-2000	2000US-0241809P	CC	supplement the patient's own production of (I). Additionally, (I)	
PR	20-OCT-2000	2000US-0241826P	CC	polynucleotides may be used to produce the secreted (I), by inserting the	
PR	01-NOV-2000	2000US-0244617P	CC	nucleic acids into a host cell and cult	

		92.0%	Score 18.4	DB 2	Length 37
Query Match		Best Local Similarity	95.0%	Pred. No. 16	
Matches	19	Conservative	0	Mismatches	1
				Indels	0
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db	8	AGTAGCCACCAAGTGTCCA	27		

Identifying modulators of untranslated region-dependent expression of a

Sequence 1192 BP; 378 A; 177 C; 169 G; 468 T; 0 U; 0 Other;

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QY      1 AATGAGCCACCAGTGTCCAA 20
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Db      49 AGTGAGCCACCAGTGTCCAA 30

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AC ADB59258;

DT 04-DEC-2003 (first entry)

Toxicity-related gene, SEQ ID 4284.

OS Unidentified

PN WO2003064624-A2.

PD 07-AUG-2003

31-JAN-2003; 2003WO-US0003194.

PR 31-JAN-2002; 2002US-00060087
DE 15-MAR-2002 03:40AED

PR 15-MAR-2002; 2002US-0364055P
 PR 30-DEC-2002; 2002US-0435543P

AA
PA
(GENE-) GENE LOGIC INC

Mendrick D. Porter M. Johnson K. Higgs B. Castle A. Eliahooff M.

DR WPI, 2003-689530/65.

PT Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays.

PT Compares preparing gene expression profile of tissue or cells exposed to the compound.

PS Claim 1; SEQ ID NO 4284; 1156pp; English.

CC The present invention relates to a method for predicting a toxic effect
CC of a compound. The method comprises preparing a gene expression profile
CC of a tissue or cell sample exposed to the compound, and comparing the
CC gene expression profile to a database comprising SEQ ID 1-4925, where

CC differential expression of the gene indicates at least one toxic effect.
 CC The method is useful for predicting at least one toxic effect of a
 CC compound, predicting hepatotoxicity or the progression of a toxic effect
 CC of a compound, identifying an agent that modulates the onset or
 CC progression of a toxic response, predicting the cellular pathways that a
 CC compound modulates in a cell, and identifying an agent that modulates at
 CC least one activity of a protein. The method and compositions of the
 CC present invention using a database of genes having liver toxin-induced
 CC differential expression, are useful in identifying toxicity markers in
 CC liver tissues or cells for drug screening and toxicity assays. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2711 BP; 798 A; 613 C; 623 G; 677 T; 0 U; 0 Other;

QY Query Match 92.0%; Score 18.4; DB 10; Length 2711;
 Best Local Similarity 95.0%; Pred. No. 30;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 AATGAGCCACCACTGTCCAA 20
 2707 AGTGAGCCACCACTGTCCAA 2688

RESULT 9

AB054551/C
 ID AB054551 standard; cDNA; 2861 BP.

XX AB054551;

XX 22-AUG-2002 (first entry)

DE Human ovarian antigen HMORJ10 cDNA, SEQ ID NO:431.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KM ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KM PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KM inflammatory condition; immune disorder; blood disorder;
 KM cardiovascular disorder; respiratory disorder; neurological disorder;
 KM gastrointestinal disorder; urinary system disorder; drug screening;
 KM gene therapy; chromosome mapping; forensic analysis;
 KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KM antiinflammatory; gynaecological; reproductive; chromosome 14q21-24;
 KM gene; 86.

XX Homo sapiens.

XX MO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Blaise CE, Rosen CA;

XX WPI; 2002-147878/19.

XX F-PsDB; ABP41474.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.

XX Claim 1; SEQ ID NO 431; 2922BP; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also

CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovarian and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents cDNA encoding a human ovarian antigen of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 2861 BP; 960 A; 539 C; 484 G; 877 T; 0 U; 1 Other;

QY Query Match 92.0%; Score 18.4; DB 6; Length 2861;
 Best Local Similarity 95.0%; Pred. No. 30;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 AATGAGCCACCACTGTCCAA 20
 1677 AGTGAGCCACCACTGTCCAA 1658

XX AD116279 standard; DNA; 3203 BP.

XX AD116279;

XX 22-APR-2004 (first entry)

DE Human nucleic acid-associated protein (NAP) coding sequence #14.

XX human; nucleic acid-associated protein; NAP; autoimmune disorder;
 KM inflammatory disorder; AIDS; allergy; infection; metabolic disorder;
 KM obesity; reproductive disorder; infertility; neurological disorder;
 KM Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KM myocardial infarction; hypertension; eye disorder;
 KM cell proliferative disease; cancer; de; gene.

XX Homo sapiens.

XX MO2003094848-A2.

XX 20-NOV-2003.

XX 09-MAY-2003; 2003WO-US014450.

XX 10-MAY-2002; 2002US-0379843P.

XX 24-MAY-2002; 2002US-0383457P.

XX 31-MAY-2002; 2002US-0384699P.

XX 06-JUN-2002; 2002US-0387265P.

XX (INCY-) INCYTE CORP.
 XX Kable AE, Elliott VS, Tran UK, Ramkumar J, Margulis JP, Chawla NK,
 XX Richardson TW, Bulloch SA, Khare R, Lee SY, Lai PG, Tang YT, Yue H;

PI Swarnakar A, Becha SD, Hafalia AJA, Chang H, Baughn MR, Boroweky ML,
 PI Gleitzen KJ, He A, Forsythe JY, Sprague WM, Blake JJ, Warren BA,
 PI Mason PM, Ison CH, Lindquist EA, Wilson AD, Jin P,
 DR WPI; 2004-011999/01.
 DR P-PsDB; AD116229.
 XX
 PT New human nucleic acid associated proteins and polynucleotides, useful
 PT for diagnosing, preventing or treating diseases or conditions associated
 PT with aberrant protein expression, e.g. cancer, AIDS, atherosclerosis or
 PT stroke.
 PS Claim 5; SEQ ID NO 64; 400bp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of human
 CC nucleic acid-associated proteins (NAP). The DNA and protein sequences of
 CC the invention are useful in diagnosing, preventing and treating
 CC diseases/conditions associated with altered expression of NAP, such as:
 CC autoimmune/inflammatory disorders (e.g. AIDS and allergies), infections
 CC (e.g. bacterial and viral), metabolic disorders (e.g. obesity),
 CC reproductive disorders (e.g. infertility), neurological disorders (e.g.
 CC Parkinson's disease and Alzheimer's disease), cardiovascular disorders
 CC (e.g. myocardial infarction and hypertension), eye disorders, or cell
 CC proliferative diseases (e.g. cancer). The present DNA sequence encodes a
 CC human NAP protein of the invention.
 XX
 SQ Sequence 3203 BP; 978 A; 691 C; 653 G; 881 T; 0 U; 0 Other;
 XX
 Query Match 92.0%; Score 18.4; DB 12; Length 3203;
 Best Local Similarity 95.0%; Pred. No. 31;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 AATGAGCCACCAAGTCCAA 20
 DB 2766 AGTGAAGCCACCAAGTCCAA 2747
 XX
 RESULT 11
 AD24506/c
 ID AD24506 standard; cDNA; 3229 BP.
 XX
 AC AD24506;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human cDNA differentially expressed in adipose tissue, INCTE1250434CBL.
 XX
 KW ss; differential expression; adipose tissue; cytosolic; hypotensive;
 KW antihypertensive; antidiabetic; anorectic; gene therapy;
 KW peroxisome proliferator-activated receptor gamma; PPARgamma;
 KW diabetes mellitus; obesity; hypertension; atherosclerosis; breast cancer;
 KW prostate cancer; colon cancer; polycystic ovarian syndrome.
 XX
 OS Homo sapiens.
 XX
 PN US2003096272-A1.
 XX
 PD 22-MAY-2003.
 XX
 PF 29-JUL-2002; 2002US-00208408.
 XX
 PR 30-JUL-2001; 2001US-0308868P.
 XX
 PA (INCY-) INCTE GENOMICS INC.
 XX
 PI Schebye XM;
 XX
 DR WPI; 2003-606416/57.
 XX
 PT New combination comprising several cDNAs, useful for preparing a
 PT composition for diagnosing or treating diabetes mellitus, obesity,
 PT hypertension, atherosclerosis, or cancer of the breast, prostate or
 PT colon.

XX
 PS Claim 1; Page 46-47; 84pp; English.
 CC
 CC Then invention relates to a new combination comprising 55 cDNAs (ADA24485
 CC -ADA24539) or their complements that are differentially regulated in an
 CC adipose sample. Also included are detecting differential expression of
 CC one or more cDNAs in a sample containing nucleic acids, screening several
 CC molecules or compounds to identify a ligand that specifically binds a
 CC cDNA, a vector comprising the cDNA, a host cell containing the vector,
 CC producing a protein, screening several molecules or compounds, producing
 CC an antibody and the isolated antibody. The cDNAs comprise sequences which
 CC are upregulated or downregulated in response to peroxisome proliferator-
 CC activated receptor gamma (PPARgamma) agonist. The combination comprising
 CC several cDNAs is useful for preparing a composition for diagnosing or
 CC treating diabetes mellitus, obesity, hypertension, atherosclerosis,
 CC cancer of the breast, prostate or colon, or polycystic ovarian syndrome.
 XX
 SQ Sequence 3229 BP; 987 A; 695 C; 658 G; 889 T; 0 U; 0 Other;
 XX
 Query Match 92.0%; Score 18.4; DB 9; Length 3229;
 Best Local Similarity 95.0%; Pred. No. 31;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 AATGAGCCACCAAGTCCAA 20
 DB 2794 AGTGAAGCCACCAAGTCCAA 2775
 XX
 RESULT 12
 ADE25615/c
 ID ADE25615 standard; cDNA; 3229 BP.
 XX
 AC ADE25615;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human cDNA differentially expressed in foam cells #19.
 XX
 KW Human; ss; differential expression; foam cell; LPS; lipopolysaccharide;
 KW cardiovascular disease; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN US2003194721-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 18-SEP-2002; 2002US-00247671.
 XX
 PR 19-SEP-2001; 2001US-0323784P.
 XX
 PA (INCY-) INCTE GENOMICS INC.
 XX
 PI Mikita T, Shiftman D, Porter JG, Kaser MR;
 XX
 DR WPI; 2003-875398/01.
 DR P-PsDB; ADE25733.
 XX
 PT Combination containing several polynucleotide that are differentially
 PT expressed in foam cells and complements of the polynucleotides, useful
 PT for diagnosing cardiovascular disease or atherosclerosis.
 XX
 PS Claim 1; SEQ ID NO 19; 37bp; English.
 XX
 CC The invention relates to a combination comprising several polynucleotides
 CC having any one of 127 sequences (SI) such as the sequence of human
 CC calmodulin gene, human mRNA for KIRA030 protein, leukotriene A₄
 CC hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit
 CC mRNA, etc., and their complements. The cDNAs are differentially expressed
 CC in LPS (lipopolysaccharide)-treated foam cells. Also included are
 CC obtaining an extended or full length gene from a library of nucleic acid
 CC sequences, an expression vector containing the nucleic acids, a host cell
 CC containing the vector, a purified polypeptide appearing as ADE25750 and

CC ADE25751, producing a protein by culturing the host cell, and a
CC composition comprising a purified antibody that specifically binds to the
CC protein. The foam cell-expressed nucleic acids are useful for a high
CC throughput detection of differential expression of one or more
CC polynucleotides in a sample. The sample is from a subject with
CC atherosclerosis and comparison with a standard defines early, mid or late
CC stages of the disorder. The foam cell-expressed nucleic acids are useful
CC for high throughput screening of a library of molecules or compounds to
CC identify a ligand which binds a polynucleotide. The library is chosen
CC from DNA molecules, peptides, proteins and RNA molecules. The protein is
CC useful for a high throughput screening of library of molecules or
CC compounds to identify at least one ligand which specifically binds a
CC protein, for purifying a ligand from a sample for making an antibody. The
CC foam cell-expressed nucleic acids are useful for diagnosing
CC cardiovascular disorder. The foam cell-expressed nucleic acids are useful
CC as elements on a microarray which can be used for detecting related
CC polynucleotides in a sample, diagnosing cardiovascular disease,
CC atherosclerosis. The present sequence represents a cDNA whose expression
CC is upregulated in LPS treated foam cells.
CC
XX

SO Sequence 3229 BP; 987 A; 695 C; 658 G; 889 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 10; Length 3229;
Best Local Similarity 95.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCACTGTCCAA 20
Db 2794 AGTGAGCCACCACTGTCCAA 2775

RESULT 13

ADJ56307/c
ID ADJ56307 standard; cDNA; 3229 BP.

AC ADJ56307;

XX 06-MAY-2004 (first entry)

DE Human cDNA differentially expressed in MYCN activated cells Segid 113.

XX human; differential expression; transactivator; proto-oncogene;

KM neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss;

XX MYCN activated cell.

OS Homo sapiens.

XX US2003119009-A1.

XX 26-JUN-2003.

XX 25-FEB-2002; 2002US-00084817.

XX 23-FEB-2001; 2001US-0270784P.

XX (STUA/) STUART S G.

XX (NUCH/) NUCHTERN J G.

XX (PLON/) PLOON S E.

XX (SHOH/) SHOHEIT J M.

XX Stuart SG, Nuchtern JG, Ploon SB, Shoheit JM;

XX WPI; 2003-635698/60.

XX New genes regulated by MYCN activation, useful in gene therapy,

XX particularly for treating a subject with e.g. neuroblastoma or other

XX cancer, or for diagnosing, staging or monitoring the treatment of the

XX cancer.

XX Claim 1; SEQ ID NO 113; 27pp; English.

XX This invention relates to novel isolated cDNAs that are differentially

XX expressed in MYCN activated cells. Specifically, it refers to

CC polynucleotide sequences that exhibit differential expression patterns in
CC cells activated by the transactivator MYCN, where MYCN is a proto-
CC oncogene that is amplified in neuroblastoma cells and is common in small
CC cell lung cancers. The present invention describes these cDNA molecules
CC as useful for in hybridisation assays to detect expression of nucleic
CC acids (or complementary nucleic acids) in a present in a given sample, as
CC well as for screening assays by identifying molecules or compounds that
CC specifically bind the cDNA as a ligand and modulate function or activity.
CC Accordingly, these compositions exhibit cytostatic activity and can also
CC be used for gene therapy purposes. This polynucleotide sequence is a cDNA
CC that is differentially expressed in MYCN activated cells, given in an
CC exemplification of the invention. NOTE: This sequence does not appear in
CC the printed specification but has been obtained in electronic format from
CC the US Patent Office at
CC ftp://seqdata.uspto.gov/sequence.html?DocID=20030119009.
CC
XX

SO Sequence 3229 BP; 987 A; 695 C; 658 G; 889 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 10; Length 3229;
Best Local Similarity 95.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCACTGTCCAA 20
Db 2794 AGTGAGCCACCACTGTCCAA 2775

RESULT 14

ADJ76983/c
ID ADJ76983 standard; cDNA; 3229 BP.

AC ADJ76983;

XX 29-JAN-2004 (first entry)

DE Human cDNA differentially expressed in a liver disorder #106.

XX human; ss; gene; liver disorder; hyperlipidaemia; hypertension;

KM type II diabetes; tumour; liver; inflammatory disorder;

KM immune response disorder; high-throughput screening;

XX differential gene expression; gene therapy.

OS Homo sapiens.

XX US2003108871-A1.

XX 12-JUN-2003.

XX 30-JUL-2001; 2001US-00919039.

XX 28-JUL-2000; 2000US-0222113P.

XX (KASE/) KASER M R.

XX Kaser MR;

XX WPI; 2004-031227/03.

XX P-PSDB; ADJ76984.

XX Composition comprising several cDNAs that are differentially expressed in

XX disorders.

XX Claim 1; SEQ ID NO 148; 41pp; English.

XX The invention relates to a composition comprising several cDNAs that are

XX differentially expressed in a liver disorder. The composition is useful

XX for treating liver disorder such as hyperlipidaemia, hypertension, type

XX II diabetes, tumours of the liver and disorders of the inflammatory and

XX immune response. The composition is useful for a high-throughput method

XX of screening several molecules or compounds to identify a ligand which

XX specifically binds a cDNA. A protein encoded by the cDNA is useful for a

XX high-throughput method for using a protein to screen several molecules or

CC compounds to identify at least one ligand which specifically binds the
CC protein which involves combining the protein encoded by the cDNA with
CC several of molecules or compounds under conditions to allow specific
CC binding, and detecting specific binding between the protein and a
CC molecule or compound, therefore identifying a ligand which specifically
CC binds the protein. The composition is useful for detecting and
CC quantifying differential gene expression, can be used in gene therapy, to
CC formulate prognosis and to design a treatment regimen and to monitor the
CC efficiency of treatment. The present sequence represents a cDNA
CC differentially expressed in a liver disorder.

XX Sequence 3229 BP; 987 A; 695 C; 658 G; 889 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 12; Length 3229;

Best Local Similarity 95.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
| | | | | | | | | | | | | | | | | | | | | |
DB 2794 AGTGAAGCCACCAAGTGTCCAA 2775

RESULT 15

ADN74945/C
ID ADN74945 standard; cDNA; 3551 BP.

XX ADN74945;

DT 12-AUG-2004 (first entry)

DE DNA encoding human hypoxia-inducible factor 1 alpha #2.

XX es; gene; human; antisense therapy; hypoxia-inducible factor 1 alpha;

XX hyperproliferative disorder.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 29..2236
/*tag= a
/product= "Hypoxia-inducible factor 1 alpha"

XX US2004101858-A1.

XX 27-MAY-2004.

XX 23-NOV-2002; 2002US-00304126.

XX 23-NOV-2002; 2002US-00304126.

XX (ISIS-) ISIS PHARM INC.

XX Ward DT, Dobie KM;

XX WPI; 2004-399686/37.

XX P-PSDB; ADN75066.

XX New compounds, particularly oligonucleotides targeted to a nucleic acid
XX encoding hypoxia-inducible factor 1 alpha, useful for treating diseases
XX associated with hypoxia-inducible factor 1 alpha, e.g. hyperproliferative
XX disorders.

XX Example 15; SEQ ID NO 13; 80bp; English.

XX The invention relates to antisense oligonucleotides targeted to, and
XX which specifically hybridize with, and inhibit expression of, a nucleic
XX acid molecule encoding hypoxia-inducible factor 1 alpha. The antisense
XX oligonucleotides are useful for treating a disease or condition
XX associated with hypoxia-inducible factor 1 alpha, such as a
XX hyperproliferative disorder. They are also useful in research and
XX diagnostics for modulating the expression of hypoxia-inducible factor 1
XX alpha. The present sequence represents DNA encoding human hypoxia-
XX inducible factor 1 alpha #2.

XX Sequence 3551 BP; 1150 A; 671 C; 650 G; 1080 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 12; Length 3551;

Best Local Similarity 95.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
| | | | | | | | | | | | | | | | | | | | | |
DB 2428 AGTGAAGCCACCAAGTGTCCAA 2409

Search completed: May 21, 2006, 21:17:47
Job time : 261.5 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using BW model

Run on: May 21, 2006, 21:16:50 ; Search time 2223.5 Seconds
(without alignments)
502.985 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagcaccagtcctccaa 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	238	7	BE764191 IL5-NT007
2	20	100.0	250	7	BE764172 IL5-NT007
3	20	100.0	255	8	CV826845 EST001143
4	20	100.0	266	7	BE764166 IL5-NT007
5	20	100.0	317	7	BE712842 MR0-HT09
6	20	100.0	327	7	BE160136 QV1-HT041
7	20	100.0	344	9	DN130625 1147199 M
8	20	100.0	375	10	DY153390 000705BMP
9	20	100.0	378	5	CD288229 3 L13.8bd
10	20	100.0	389	10	DY112562 000222BOV
11	20	100.0	394	4	BE925260 CM4-AN008
12	20	100.0	403	4	CA778645 MFL384.10
13	20	100.0	492	10	DY769093 ILUMIGEN
14	20	100.0	537	1	AJ683529 MR2-NT013
15	20	100.0	545	2	BE923330 MR2-NT013
16	20	100.0	560	9	CX593021 CT020003B
17	20	100.0	591	9	DN402969 LIB4004-0
18	20	100.0	596	9	DA541613 DA541613
19	20	100.0	613	10	DY085271 001022BUT

c 20	20	100.0	634	8	CK978607	CK978607	4110096 B
c 21	20	100.0	653	5	CK947392	CK947392	4071959 B
c 22	20	100.0	657	8	CN264295	CN264295	17006000
c 23	20	100.0	661	1	AJ746976	AJ746976	17006000
c 24	20	100.0	681	1	CB118713	CB118713	K-EST015
c 25	20	100.0	683	7	BF042862	BF042862	BP250019B
c 26	20	100.0	696	5	CK962009	CK962009	4076289 B
c 27	20	100.0	696	10	DT895390	DT895390	1478415 M
c 28	20	100.0	701	9	DN395152	DN395152	LIB3935-0
c 29	20	100.0	725	1	AJ955413	AJ955413	170004277
c 30	20	100.0	726	8	CN264320	CN264320	170004277
c 31	20	100.0	737	4	CD103310	CD103310	AGENCOURT
c 32	20	100.0	750	1	AV702635	AV702635	AGENCOURT
c 33	20	100.0	751	2	BG112073	BG112073	602283241
c 34	20	100.0	753	10	DV830978	DV830978	LB01917.C
c 35	20	100.0	772	4	CB312460	CB312460	AGENCOURT
c 36	20	100.0	786	9	DN425733	DN425733	LIB4216-0
c 37	20	100.0	788	4	CD110467	CD110467	AGENCOURT
c 38	20	100.0	788	5	CJ462062	CJ462062	AGENCOURT
c 39	20	100.0	804	10	DV873369	DV873369	LB02520.C
c 40	20	100.0	818	2	BG108056	BG108056	602279983
c 41	20	100.0	824	1	AJ950688	AJ950688	170004277
c 42	20	100.0	835	10	DV834747	DV834747	LB0196.C
c 43	20	100.0	861	1	AJ945476	AJ945476	170004277
c 44	20	100.0	908	10	DV921086	DV921086	LB02923.C
c 45	20	100.0	923	2	BG108209	BG108209	602280087

ALIGNMENTS

RESULT 1
BE764191/c 238 bp mRNA linear EST 19-SEP-2000
LOCUS IL5-NT0071-200600-106-h11 NT0071 Homo sapiens CDNA, mRNA sequence.
DEFINITION BE764191
ACCESSION BE764191
VERSION BE764191.1 GI:10194115
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 238)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.J.F., Zago,M.A., Bordin,S., Costa,F.E., Goldman,G.H., Carvalho,A.F., Matsumura,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2-IL5-NT0071-200600-106-h11&t3=2000-06-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 59
High quality sequence stop: 238.
Location/Qualifiers
1. 238
/organism="Homo sapiens"
/mol_type="mRNA"

```

/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0071"
/notes="Organ: nervous tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

ORIGIN

```

Query Match      100.0%; Score 20; DB 7; Length 238;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTAA 20
    |||||
Db 156 AATGAGCCACCAGTGTCCTAA 137

```

RESULT 2

```

LOCUS BE764172 250 bp mRNA linear EST 19-SEP-2000
DEFINITION IL5-NT0071-200600-106-c10 NT0071 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE764172
VERSION BE764172.1 GI:10194096
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

REFERENCE

```

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

```

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=IL5-NT0071-200
600-106-c10&t3=2000-06-20&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 250.

FEATURES

source

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1. .250
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0071"

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```

/notes="Organ: nervous tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

ORIGIN

```

Query Match      100.0%; Score 20; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTAA 20
    |||||
Db 83 AATGAGCCACCAGTGTCCTAA 102

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RESULT 3

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LOCUS CV826845/c 255 bp mRNA linear EST 13-DEC-2004
DEFINITION Japonicus cDNA clone SJ15D12, mRNA sequence.
ACCESSION CV826845
VERSION CV826845.1 GI:55776384
KEYWORDS EST.
SOURCE Gekko japonicus
ORGANISM Gekko japonicus

```

```

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
Gu,X., Ding,F., Liu,Y., Liu,M., Shen,M., Gong,L., Zhang,Q., Tang,X.
and Yang,H.

```

TITLE

Analysis of expressed sequences tags and cloning of full length
cDNA from brain and spinal cord cDNA library in Gecko (2004)

JOURNAL

COMMENT

Contact: Gu Xiaosong
The Key Laboratory of Neuroregeneration of Jiangsu Province
Nantong Medical College
Qixiu Road 19, Nantong city, Jiangsu Province, P.R.China
Tel: 86-513-5051800
Fax: 86-513-5511585
Email: neuron@public.nt.js.cn.

FEATURES

source

```

1. .255
/organism="Gekko japonicus"
/mol_type="mRNA"
/db_xref="taxon:146911"
/clone="SJ15D12"
/tissue_type="brain and spinal cord"
/clone_lib="brain and spinal cord cDNA library in Gecko"

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ORIGIN

```

Query Match      100.0%; Score 20; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTAA 20
    |||||
Db 234 AATGAGCCACCAGTGTCCTAA 215

```

RESULT 4

```

LOCUS BE764166/c 266 bp mRNA linear EST 19-SEP-2000
DEFINITION IL5-NT0071-200600-106-b05 NT0071 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE764166
VERSION BE764166.1 GI:10194090
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

```

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

```

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBLISHED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=IL5-NT0071-200>)
 600-106-b05et3=2000-06-20et4=1
 Seq primer: puc 18 forward
 High quality sequence stop: 266.
FEATURES
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 1. 266
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0071"
 /notes="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
 Query Match 100.0%; Score 20; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AATGAGCCACCACTGTCCAA 20
 |||||
 Db 168 AATGAGCCACCACTGTCCAA 149
RESULT 5
LOCUS BE712842 317 bp mRNA linear EST 12-SEP-2000
DEFINITION MRO-HT0699-060800-001-h09 HT0699 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE712842
VERSION BE712842.1 GI:10101107
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 317)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBLISHED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=MR0-HT0699-060>)
 800-001-h09et3=2000-08-06et4=1
 Seq primer: puc 18 forward
 High quality sequence start: 14
 High quality sequence stop: 317.
FEATURES
 source
 1. 317
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="HT0699"
 /notes="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
 Query Match 100.0%; Score 20; DB 7; Length 317;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AATGAGCCACCACTGTCCAA 20
 |||||
 Db 149 AATGAGCCACCACTGTCCAA 168
RESULT 6
LOCUS BE160136 327 bp mRNA linear EST 21-JUN-2000
DEFINITION QV1-HT0412-290400-178-h08 HT0412 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE160136
VERSION BE160136.1 GI:8622857
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 327)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBLISHED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=QV1-HT0412-290>)
 400-178-h08et3=2000-04-29et4=1
 Seq primer: puc 18 forward
 High quality sequence stop: 78.
FEATURES
 source
 1. 327
 Location/Qualifiers
 /organism="Homo sapiens"

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0412"
/notes="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (O.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

ORIGIN

```

Query Match      100.0%; Score 20; DB 7; Length 327;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AATGAGCCACCAAGTGTCCTAA 20
    |||||
Db 63 AATGAGCCACCAAGTGTCCTAA 82

```

RESULT 7

```

LOCUS      DNI130625      344 bp      mRNA      linear      EST 15-FEB-2005
DEFINITION 1147199 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
ACCESSION  DNI130625
VERSION     DNI130625.1 GI:59824906
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 344)
Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.E. and Keele,J.W.
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2003)
Contact: Smith,TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_al option. Vector identified with
cross match v0.990329.
Plate: HHY8037 row: A column: 11
Seq primer: TAGAGCGACAGTCGAGG.

```

FEATURES

```

source
1..344
Location/Qualifiers
1..344
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 4PIG"
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

```

ORIGIN

```

Query Match      100.0%; Score 20; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AATGAGCCACCAAGTGTCCTAA 20
    |||||
Db 98 AATGAGCCACCAAGTGTCCTAA 117

```

RESULT 8

```

LOCUS      DY153390/c      375 bp      mRNA      linear      EST 01-FEB-2006
DEFINITION 000705EMPA002625HT BMPA Bos taurus cDNA, mRNA sequence.
ACCESSION  DY153390
VERSION     DY153390.1 GI:86347565
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
ORGANISM    Bos taurus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 375)
McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
Hagemann,L., Lee,R., Hein,W., Johnstone,P., Macphail,N., McMahon,C.,
McCracken,J., Steiwen,K., Farr,V., Singh,K., Whitley,J.,
Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
Wells,M., Bowman,P., Goddard,M., Langford,C., McSwan,J. and
Atkinson,P.
AgResearch, Genesis and Primary Industry Victoria Bovine EST
Project
Unpublished (2006)
Contact: Macphail N
AgResearch Ltd.
Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
Mossiel, New Zealand
Email: nauman.macphail@agresearch.co.nz.

```

```

TITLE      AgResearch, Genesis and Primary Industry Victoria Bovine EST
JOURNAL
COMMENT

```

FEATURES

```

source
1..375
Location/Qualifiers
1..375
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Pre-Partum mammary"
/clone_lib="BMPA"
/notes="Vector: pBK-CMV; Bovine 85 days pre-partum mammary
tissue cDNA library derived from tissue harvested from an
Angus cow by Adrian Molenaar on 01/01/00"

```

ORIGIN

```

Query Match      100.0%; Score 20; DB 10; Length 375;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AATGAGCCACCAAGTGTCCTAA 20
    |||||
Db 78 AATGAGCCACCAAGTGTCCTAA 59

```

RESULT 9

```

LOCUS      CD288229/c      378 bp      mRNA      linear      EST 27-MAY-2003
DEFINITION 3.Li3.abd POE14_Day_14_pregnant_ovine_endometrium) Ovis aries
cDNA, mRNA sequence.
ACCESSION  CD288229
VERSION     CD288229.1 GI:31086272
KEYWORDS    EST.
SOURCE      Ovis aries (sheep)
ORGANISM    Ovis aries

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
1 (bases 1 to 378)
Gray,C.A., Abbey,C.A., Beremand,P.D., Choi,Y., Farmer,J.L.,
Adelson,D.L., Thomas,I.L., Bazer,F.W. and Spencer,T.E.
Identification of Endometrial Genes Regulated by Early Pregnancy,
Progesterone, and Interferon Tau in the Ovine Uterus
Biol. Reprod. 74 (2), 383-394 (2006)
16251498
Contact: Thomas E. Spencer
Center for Animal Biotechnology and Genomics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,

```


USA
Tel: 9798454896
Fax: 9798622862
Email: tepencer@ansc.tamu.edu.

FEATURES

source

Location/Qualifiers

1. .378
/organism="Ovis aries"
/mol_type="mRNA"
/db_xref="taxon:9940"
/sex="Female"
/tissue_type="endometrium"
/dev_stage="Day 14 pregnant"
/clone_lib="POE14 (Day 14 pregnant ovine endometrium)"
/note="Organ: uterus; Vector: Triplex2; Site 1: EcorI; Site 2: XhoI; Non-normalized library, sequenced 5' with Triplex2 primer (CTCCGATCTGCAGCAGC). Library constructed by Clontech with total RNA extracted using the Trizol method and pooled from 5 females."

ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 378;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCACTGTCCAA 20

Db 351 AATGAGCCACCACTGTCCAA 332

RESULT 10

DY112562/c

LOCUS DY112562 389 bp mRNA linear EST 01-FEB-2006
DEFINITION 000222BOVB005432HT BOVB Bos taurus CDNA, mRNA sequence.
ACCESSION DY112562
VERSION DY112562.1 GI:86275839
KEYWORDS EST.

SOURCE

Bos taurus (cattle)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 389)

AUTHORS

McClulloch, A., Wilson, T., Molenaar, A., Grigor, M., Davis, S.,
Glenn, M., Havukkala, I., Watson, J., Crawford, A., Wheeler, T.,
Hagemann, L., Lee, R., Hein, W., Johnstone, P., Macgibbon, N., McMahon, C.,
McCracken, J., Stelwagen, K., Farr, V., Singh, K., Whitley, J.,
Nicholas, K., Savin, K., Mather, A., McPartlan, H., Whitley, J.,
Wells, M., Bowman, P., Goddard, M., Langford, C., McEwan, J. and
Atkinson, P.

AgResearch, Genesis and Primary Industry Victoria Bovine EST

PROJECT

Unpublished (2006)

Contact: Macgibbon N

AgResearch Ltd.

Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,

Mosgiel, New Zealand

Email: nauman.macgibbon@agresearch.co.nz.

FEATURES

source

Location/Qualifiers

1. .389
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Ovarian"
/clone_lib="BOVB"
/notes="Vector: pBK-CMV; Bovine ovary cDNA library derived from tissue harvested from an unknown breed calf by Allan Crawford on 28/09/99"

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCACTGTCCAA 20

Db 152 AATGAGCCACCACTGTCCAA 133

RESULT 11

BE925260

LOCUS BE925260

DEFINITION

BE925260

ACCESSION

BE925260.1

VERSION

BE925260.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 394)

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,

Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

10737800

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=CM4-AN0081-210

800-274-d01st3=2000-08-21&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 24

High quality sequence stop: 392.

FEATURES

source

Location/Qualifiers

1. .394

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="AN0081"

/notes="Organ: amnion normal; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 394;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCACTGTCCAA 20

Db 89 AATGAGCCACCACTGTCCAA 108

RESULT 12

CAY78645/c

LOCUS CAY78645

DEFINITION

CAY78645

ACCESSION

MPL384_10_D22 MPL Sus scrofa cDNA clone pSPOR1 5', mRNA sequence.


```

VERSION CA778645.1 GI:26016521
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1 (bases 1 to 403)
AUTHORS Center for Animal Functional Genomics.
TITLE Generation of ESTs from mixed pig cDNA libraries
JOURNAL Unpublished (2002)
COMMENT Contact: Steven P. Suchyta
Center for Animal Functional Genomics, Department of Animal Science
Michigan State University
B215 Anthony Hall, East Lansing, MI 48824, USA
Tel: 517 355 8443
Fax: 517 432 9168
Email: suchytas@msu.edu
Single pass sequencing. Bases called and alt-trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore
20 -minmatch 12 options.
Seq primer: T7.
Location/Qualifiers
1..403
/organism="Sus scrofa"
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/db_xref="taxon:9823"
/clone="pSPORT1"
/sex="Male and female"
/tissue_type="pooled"
/dev_stage="pooled"
/lab_host="DH10B"
/clone_lib="WPL"
/notes="Organ: pooled; Vector: pSPORT1; Site 1: Not I;
Site 2: Sal I; Library made from pooled tissue from
adipose, adrenal gland, blood leukocytes, brain,
cartilage, eye, heart, intestine, kidney, liver, lung
lymph nodes, mammary gland, myogenic satellite cells,
ovary, pancreas, pituitary gland, placenta, skin, spinal
cord, spleen, stomach, tendon, testes, uterus, and
vascular from various developmental and physiological
stages."

ORIGIN
Query Match 100.0%; Score 20; DB 4; Length 403;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACAGTGTCCAA 20
|||||
Db 216 AATGAGCCACAGTGTCCAA 197

RESULT 13
LOCUS DV769093/c
DEFINITION ILLUMIGEN MCQ 67822 Katze MWTE Macaca mulatta cDNA clone
|BIUW:39154 57 similar to Bases 5 to 392 highly similar to human
|HFLA (Hs.509554), mRNA sequence.
DV769093 492 bp mRNA linear EST 22-NOV-2005
ILLUMIGEN MCQ 67822 Katze MWTE Macaca mulatta cDNA clone
|BIUW:39154 57 similar to Bases 5 to 392 highly similar to human
|HFLA (Hs.509554), mRNA sequence.
DV769093.1 GI:82613035
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SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 492)
AUTHORS Magnus, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agv, M.B.,
Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.
TITLE Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human

JOURNAL PUBMED
COMMENT Genome Biol. 6 (7), R60 (2005)
15998449
Contact: C. Magnus
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnus@illumigen.com
Sequenced on 2005.08.01. 669 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
PCR Primers
FORWARD: CCTCTACTAAGGGAACAAAA
BACKWARD: CACTATAGGCGGAAATGGGTA
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/clone="IBIUW:39154"
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/tissue_type="testis"
/dev_stage="juvenile"
/lab_host="Electromax DH10B"
/clone_lib="Katze MWTE"
/notes="Vector: pDONR 222; Site 1: BsrG I; Site 2: BsrG I;
Created from CloneMiner cDNA Library Construction kit
(catalog #18249-029)"

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Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 417 AATGAGCCACAGTGTCCAA 398

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sequence.
ACCESSION AJ683529
VERSION AJ683529.1 GI:49416119
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 537)
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector: pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13P Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,

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    EH25 9PS, www.arkgenomics.org.
    Location/Qualifiers
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        /note="Vector: pALuescriptII(KS+); Site 1: EcoRI; Site 2:
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  DB      214 AATGAGCCACCAGTGTCCAA 195
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LOCUS
DEFINITION MR2-NT0137-211100-005-a08 NT0137 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF923330
VERSION BF923330.1 GI:12319218
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  AUTHORS
    1 (bases 1 to 545)
    Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
    Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
    Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
    Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
    O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
    Simpson, A.J.
    Shotgun sequencing of the human transcriptome with ORF expressed
    sequence tags
    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
    10737800
  CONTACT: Simpson A.J.G.
  Laboratory of Cancer Genetics
  Ludwig Institute for Cancer Research
  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
  Brazil
  Tel: +55-11-2704922
  Fax: +55-11-2707001
  Email: asimpson@ludwig.org.br
  This sequence was derived from the FAPESP/LICR Human Cancer Genome
  Project. This entry can be seen in the following URL
  (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&st2=MR2-NT0137-
  211100-005-a08&t3=2000-11-21&t4=1)
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  High quality sequence stop: 543.
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      /db_xref="taxon:9606"
      /dev_stage="Adult"
      /clone_lib="NT0137"
      /note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
      Site 2: SmaI; A mini-library was made by cloning products
      derived from ORESTES PCR (U.S. Letters Patent application
      No. 196,716 - Ludwig Institute for Cancer Research)
      profiles into the puc 18 vector. Reverse transcription of
      tissue mRNA and cDNA amplification were performed under
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:18:10 ; Search time 79.5 Seconds
(without alignments)
470.719 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtgtccaa 20

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A-COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B-COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7-COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H-COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PTUS-COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP-COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE-COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.6	100.0	601	3	US-09-949-016-22571
C 2	19.6	100.0	601	3	US-09-949-016-52342
C 3	18.4	92.0	37	3	US-09-579-897-2
C 4	18.4	92.0	311	3	US-09-621-976-17247
C 5	18.4	92.0	601	3	US-09-949-016-22570
C 6	18.4	92.0	601	3	US-09-949-016-52341
C 7	18.4	92.0	2770	3	US-09-949-016-1518
C 8	18.4	92.0	3229	3	US-09-919-035-148
C 9	18.4	92.0	3678	3	US-09-380-662-22
C 10	18.4	92.0	3678	3	US-09-959-8738-19
C 11	18.4	92.0	3678	3	US-10-028-158-22
C 12	18.4	92.0	3736	2	US-08-480-4738-1
C 13	18.4	92.0	3736	3	US-08-915-213-1
C 14	18.4	92.0	3736	3	US-09-148-547-1
C 15	18.4	92.0	3736	3	US-09-235-217-1
C 16	18.4	92.0	3736	3	US-09-383-581-1
C 17	18.4	92.0	3736	7	PCR-US96-10251-1
C 18	18.4	92.0	3933	3	US-09-949-016-218
C 19	18.4	92.0	18120	3	US-09-949-016-13260
C 20	18.4	92.0	56714	3	US-09-949-016-11960
C 21	16.4	82.0	3924	3	US-09-023-655-1168
C 22	16.4	82.0	3924	3	US-09-762-195-2
C 23	16.4	82.0	3924	4	US-09-880-107-2299

ALIGNMENTS

RESULT 1

US-09-949-016-22571/c
; Sequence 22571, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22571
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-22571

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Qy 1 AATGAGCCACCAGTGTCCAA 20

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Db 302 ARTGAGCCACCAGTGTCCAA 283

RESULT 2

US-09-949-016-52342/c
; Sequence 52342, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

Sequence 12742, A
Sequence 15576, A
Sequence 14720, A
Sequence 1064, Ap
Sequence 41, Appl
Sequence 19, Appl
Sequence 1, Appl
Sequence 16080, A
Sequence 115253,
Sequence 115254,
Sequence 115255,
Sequence 115299,
Sequence 115300,
Sequence 14893, A
Sequence 13846, A
Sequence 12271, A
Sequence 16976, A
Sequence 16977, A
Sequence 12537, A
Sequence 14896, A
Sequence 176526,
Sequence 180123,

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/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52342
/ LENGTH: 601
/ TYPE: DNA
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US-09-949-016-52342

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Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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US-09-579-897-2
/ Sequence 2, Application US/09579897
/ Patent No. 6432927
/ GENERAL INFORMATION:
/ APPLICANT: Gregory, Richard
/ APPLICANT: Vincent, Karen
/ TITLE OF INVENTION: Compositions and Methods for Inducing Gene Expression
/ FILE REFERENCE: GA0112CIP2
/ CURRENT APPLICATION NUMBER: US/09/579,897
/ CURRENT FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/067,546
/ PRIOR FILING DATE: 1997-12-04
/ PRIOR APPLICATION NUMBER: PCT/US98/25753
/ PRIOR FILING DATE: 1998-12-04
/ PRIOR APPLICATION NUMBER: 09/133,612
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 37
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-579-897-2

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RESULT 4
US-09-621-976-17247/c
/ Sequence 17247, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 17247
/ LENGTH: 311
/ TYPE: DNA

/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
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/ NUMBER OF SEQ ID NOS: 207012
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US-09-949-016-52342

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RESULT 3
US-09-579-897-2
/ Sequence 2, Application US/09579897
/ Patent No. 6432927
/ GENERAL INFORMATION:
/ APPLICANT: Gregory, Richard
/ APPLICANT: Vincent, Karen
/ TITLE OF INVENTION: Compositions and Methods for Inducing Gene Expression
/ FILE REFERENCE: GA0112CIP2
/ CURRENT APPLICATION NUMBER: US/09/579,897
/ CURRENT FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/067,546
/ PRIOR FILING DATE: 1997-12-04
/ PRIOR APPLICATION NUMBER: PCT/US98/25753
/ PRIOR FILING DATE: 1998-12-04
/ PRIOR APPLICATION NUMBER: 09/133,612
/ PRIOR FILING DATE: 1998-08-13
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/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-579-897-2

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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4
US-09-621-976-17247/c
/ Sequence 17247, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 17247
/ LENGTH: 311
/ TYPE: DNA

/ ORGANISM: Homo sapiens
US-09-621-976-17247

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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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/ Sequence 22570, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 22570
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-22570

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RESULT 6
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/ Sequence 52341, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52341
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-52341

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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 9
US-09-380-662-22/c
; Sequence 22, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USMO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(2509)
US-09-380-662-22

Query Match          92.0%; Score 18.4; DB 3; Length 3678;
Best Local Similarity 95.0%; Pred.No.6.8;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCAA 20
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Db 2555 AGTGAGCCACCAGTGTCCAA 2536

RESULT 10
US-09-959-873B-19/c
; Sequence 19, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Threoto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-959-873B-19

Query Match          92.0%; Score 18.4; DB 3; Length 3678;
Best Local Similarity 95.0%; Pred.No.6.8;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2555 AGTGAGCCACCAGTGTCCAA 2536

RESULT 11
US-10-028-158-22/c

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Sequence 22, Application US/10028158
Patent No. 6863880
GENERAL INFORMATION:
APPLICANT: Caniggia, Isabella
APPLICANT: Post, Martin
APPLICANT: Lye, Stephen
TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
FILE OF INVENTION: TROPHOBLAST
FILE REFERENCE: 11757.38USWO
CURRENT APPLICATION NUMBER: US/10/028.158
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US/09/380,662
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: PCT/CA98/00180
PRIOR FILING DATE: 1998-03-05
PRIOR APPLICATION NUMBER: US 60/039,919
PRIOR FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent in version 3.0
SEQ ID NO 22
LENGTH: 3678
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (29)..(2509)
US-10-028-158-22

Query Match 92.0%; Score 18.4; DB 3; Length 3678;
Best Local Similarity 95.0%; Pred. No. 6.8;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20
DB 2555 AGTGAGCCACCAGTGTCCTCA 2536

RESULT 12
US-08-480-473B-1/c
Sequence 1, Application US/08480473B
Patent No. 5882914
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,473B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3736 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-480-473B-1

Query Match 92.0%; Score 18.4; DB 2; Length 3736;
Best Local Similarity 95.0%; Pred. No. 6.8;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20
DB 2555 AGTGAGCCACCAGTGTCCTCA 2536

RESULT 13
US-08-915-213-1/c
Sequence 1, Application US/08915213
Patent No. 6020462
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,213
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3736 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-915-213-1

Query Match 92.0%; Score 18.4; DB 3; Length 3736;
Best Local Similarity 95.0%; Pred. No. 6.8;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20
DB 2555 AGTGAGCCACCAGTGTCCTCA 2536

RESULT 14
US-09-148-547-1/c
Sequence 1, Application US/09148547
Patent No. 6124131
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
FILE REFERENCE: 07265/151001

Search completed: May 21, 2006, 21:21:00
Job time : 81.5 secs

; CURRENT APPLICATION NUMBER: US/09/148,547
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(2509)
US-09-148-547-1

Query Match 92.0%; Score 18.4; DB 3; Length 3736;
Best Local Similarity 95.0%; Pred. No. 6.8;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGCCAA 20
DB 2555 AGTGAGCCACCAGTGCCAA 2536

RESULT 15

US-09-235-217-1/c
; Sequence 1, Application US/09235217
; Patent No. 6222018
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,217
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3736 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-235-217-1

Query Match 92.0%; Score 18.4; DB 3; Length 3736;
Best Local Similarity 95.0%; Pred. No. 6.8;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGCCAA 20
DB 2555 AGTGAGCCACCAGTGCCAA 2536

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:21:21 ; Search time 823 Seconds
(without alignments)
298.606 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtgtccaa 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18922170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	20	100.0	20	8	US-10-766-185-2
C 3	20	100.0	57500	9	US-10-719-370A-11
C 4	20	100.0	57501	8	US-10-304-126-11
C 5	19.6	100.0	1558	4	US-09-925-065A-706976
C 6	19.6	100.0	1558	5	US-09-925-065A-706976
C 7	18.4	92.0	37	6	US-10-190-394-2
C 8	18.4	92.0	375	8	US-10-242-535A-41677
C 9	18.4	92.0	375	8	US-10-085-783A-41677
C 10	18.4	92.0	1400	10	US-10-956-157-5878
C 11	18.4	92.0	2861	7	US-10-264-049-431
C 12	18.4	92.0	3180	7	US-10-425-784-3
C 13	18.4	92.0	3229	3	US-09-919-039-148
C 14	18.4	92.0	3229	6	US-10-208-408-22
C 15	18.4	92.0	3229	6	US-10-084-817-113
C 16	18.4	92.0	3229	7	US-10-247-671-19
C 17	18.4	92.0	3551	8	US-10-304-126-13

C 18	18.4	92.0	3551	9	US-10-719-370A-13
C 19	18.4	92.0	3678	6	US-10-028-158-22
C 20	18.4	92.0	3678	9	US-10-901-583-19
C 21	18.4	92.0	3678	10	US-10-007-253-3
C 22	18.4	92.0	3678	13	US-11-043-493-22
C 23	18.4	92.0	3736	7	US-10-423-419-1
C 24	18.4	92.0	3736	10	US-10-831-380-1
C 25	18.4	92.0	3812	9	US-10-699-557-3
C 26	18.4	92.0	3927	3	US-09-813-790-231
C 27	18.4	92.0	3933	7	US-10-172-118-625
C 28	18.4	92.0	3933	7	US-10-388-360-309
C 29	18.4	92.0	3933	8	US-10-342-887-625
C 30	18.4	92.0	3933	8	US-10-407-807-1
C 31	18.4	92.0	3933	8	US-10-304-126-4
C 32	18.4	92.0	3933	9	US-10-719-370A-4
C 33	18.4	92.0	3933	9	US-10-719-370A-133
C 34	18.4	92.0	3933	9	US-10-848-646-3
C 35	18.4	92.0	3933	10	US-10-956-157-643
C 36	18.4	92.0	3933	10	US-10-494-800-59
C 37	18.4	92.0	3933	16	US-11-288-720-1
C 38	18.4	92.0	3958	9	US-10-699-557-2
C 39	18.4	92.0	4162	10	US-10-450-763-20862
C 40	18.4	92.0	4656	6	US-10-044-090-284
C 41	18	90.0	20	9	US-10-719-370A-187
C 42	18	90.0	3718	6	US-10-205-342-14
C 43	18	90.0	3718	9	US-10-699-557-4
C 44	18	90.0	3947	10	US-10-764-420-2663
C 45	18	90.0	3973	9	US-10-699-557-5

ALIGNMENTS

RESULT 1

US-10-766-185-1/c

- ; Sequence 1, Application US/10766185
- ; Publication No. US20040152655A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Yoon, Heejeong
- ; APPLICANT: Ahn, Chang Ho
- ; APPLICANT: Lee, Young Bok
- ; APPLICANT: Mao, Lingjun
- ; APPLICANT: Jiang, Xiaomeng
- ; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIP-1
- ; FILE REFERENCE: REX 7034
- ; CURRENT APPLICATION NUMBER: US/10766,185
- ; CURRENT FILING DATE: 2004-01-28
- ; NUMBER OF SEQ ID NOS: 130
- ; SOFTWARE: PatentIn version 3.1
- ; SEQ ID NO 1
- ; LENGTH: 20
- ; TYPE: DNA
- ; ORGANISM: human
- ; US-10-766-185-1

Query Match 100.0%; Score 20; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCAA 20

DB 20 AATGAGCCACCAGTGTCCAA 1

RESULT 2

US-10-766-185-2

- ; Sequence 2, Application US/10766185
- ; Publication No. US20040152655A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Yoon, Heejeong
- ; APPLICANT: Ahn, Chang Ho
- ; APPLICANT: Lee, Young Bok
- ; APPLICANT: Mao, Lingjun


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/ APPLICANT: Jiang, Xiaoming
/ TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIP-1
/ FILE REFERENCE: REX 7034
/ CURRENT APPLICATION NUMBER: US/10/766,185
/ CURRENT FILING DATE: 2004-01-28
/ NUMBER OF SEQ ID NOS: 130
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: antisense oligonucleotide
US-10-766-185-2

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Query Match      100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AATGAGCCACCAGTGTCCAA 20
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Db 1 AATGAGCCACCAGTGTCCAA 20

RESULT 3

US-10-719-370A-11/c
; Sequence 11, Application US/10719370A
; Publication No. US20040220393A1

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: GENERAL INFORMATION:
: APPLICANT: Ward, Donna T.
: APPLICANT: Dobie, Kenneth W.
: APPLICANT: Marcussen, Eric G.
: APPLICANT: Frier, Susan M.
: TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
: FILE REFERENCE: ISPT-1010
: CURRENT APPLICATION NUMBER: US/10/719,370A
: CURRENT FILING DATE: 2003-11-21
: PRIOR APPLICATION NUMBER: US 10/304,126
: PRIOR FILING DATE: 2002-11-23
: NUMBER OF SEQ ID NOS: 458
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 11
: LENGTH: 57500

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(57500)

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; ; OTHER INFORMATION: Positions 82000 to 139500 of the sequence with GenBank Accession
; ; OTHER INFORMATION: No. AL137129.4
; ; PUBLICATION INFORMATION:
; ; DATABASE ACCESSION NUMBER: AL137129.4
; ; DATABASE ENTRY DATE: 2001-04-30
; ; RELEVANT RESIDUES: (1)..(57500)
US-10-719-370A-11

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Query Match 100.0%; Score 20; DB 9; Length 57500;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0

Qy 1 AATGAGCCACCAGTGTCCAA 20
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54374 AATGAGCCACCAGTGTCCAA 54355
Db

RESULT 4

US-10-304-126-11/c
; Sequence 11, Application US/10304126
; Publication No. US20040101858A1

; GENERAL INFORMATION:
 ; APPLICANT: Donna T. Ward
 ; APPLICANT: Kenneth W. D

TITLE OF INVENTION: MODULATION OF HYPOXIA-INDUCIBLE FACTOR 1 ALPHA EXPRESSION

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; FILE REFERENCE: PTS-0070
; CURRENT APPLICATION NUMBER: US/10/304,126
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 11
; LENGTH: 57501
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-304-126-11

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Query Match 100.0%; Score 20; DB 8; Length 57501;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0

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54375 AATGAGCCACCAGTGTCCAA 54356
Db

RESULT 5

US-09-925-065A-706976/c
; Sequence 706976, Application US/09925065A
; Publication No. US20040181048A1

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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 706976
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-706976

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Query Match      100.0%; Score 20; DB 4; Length 1558;
Best Local Similarity 95.0%; Pred. No. 8.2;
Matches 19; Conservative 1; Mismatches 0; Gaps 0;
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QY 1 AATGAGCCACCAGTGTCCAA 20
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Dp 33 ARTGAGCCACCAGTGTCCAA 14

RESULT 6

US-09-925-065A-706976/c
; Sequence 706976, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:

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1 / APPLICANT: wang, David G.
2 / TITLE OF INVENTION: Identification and Mapping of Single
3 / Nucleotide Polymorphisms in the Human Genome
4 / FILE REFERENCE: 108627.135
5 / CURRENT APPLICATION NUMBER: US/09/925,065A
6 / PRIORITY FILING DATE: 2001-08-08
7 / PRIOR APPLICATION NUMBER: US 60/243,096
8 / PRIOR FILING DATE: 2000-10-24
9 / PRIOR APPLICATION NUMBER: US 60/252,147
10 / PRIOR FILING DATE: 2000-11-20
11 / PRIOR APPLICATION NUMBER: US 60/250,092

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; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 706976
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-706976

Query Match 100.0%; Score 20; DB 5; Length 1558;
Best Local Similarity 95.0%; Pred. No. 8.2;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20
|:|||||||||||||||||
Db 33 ARTGAGCCACCAAGTGTCCTAA 14

RESULT 7

US-10-190-394-2
; Sequence 2, Application US/10190394
; Publication No. US20030018007A1
; GENERAL INFORMATION:
; APPLICANT: Gregory, Richard
; APPLICANT: Vincent, Karen
; TITLE OF INVENTION: Compositions and Methods for Inducing Gene
; FILE REFERENCE: GA0112CIP2
; CURRENT APPLICATION NUMBER: US/10/190,394
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/579,897
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/067,546
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/25753
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 09/133,612
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-190-394-2

Query Match 92.0%; Score 18.4; DB 6; Length 37;
Best Local Similarity 95.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20
|:|||||||||||||||||
Db 8 AGTGAGCCACCAAGTGTCCTAA 27

RESULT 8

US-10-242-535A-41677/c
; Sequence 41677, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41677
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-41677

Query Match 92.0%; Score 18.4; DB 8; Length 375;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20
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Db 165 AGTGAGCCACCAAGTGTCCTAA 146

RESULT 9

US-10-085-783A-41677/c
; Sequence 41677, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41677
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-41677

Query Match 92.0%; Score 18.4; DB 8; Length 375;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20
|:|||||||||||||||||
Db 165 AGTGAGCCACCAAGTGTCCTAA 146

RESULT 10

US-10-956-157-5878/c
; Sequence 5878, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5878
; LENGTH: 1400
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-956-157-5878

Query Match          92.0%; Score 18.4; DB 10; Length 1400;
Best Local Similarity 95.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTCA 20
DB 258 AGTGAGCCACCAAGTGTCCTCA 239

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US-10-264-049-431/c
; Sequence 431, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PCT/US01/18569
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR FILING DATE: 2001-06-07
; PRIOR FILING DATE: 2001-06-07
; PRIOR FILING DATE: 2001-06-07
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 431
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2853)..(2853)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-431

Query Match          92.0%; Score 18.4; DB 7; Length 2861;
Best Local Similarity 95.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTCA 20
DB 1677 AGTGAGCCACCAAGTGTCCTCA 1658

RESULT 12
US-10-425-784-3/c
; Sequence 3, Application US/10425784
; Publication No. US20040009591A1
; GENERAL INFORMATION:
; APPLICANT: Comer, Allen
; APPLICANT: Hoffmann, Michael
; APPLICANT: Allen-Hoffmann, Lynn
; TITLE OF INVENTION: Keratinocytes Expressing Exogenous Angiogenic Growth Factors
; FILE REFERENCE: STRATA-08110
; CURRENT APPLICATION NUMBER: US/10/425,784
; CURRENT FILING DATE: 2003-04-29
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3180
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-425-784-3

Query Match          92.0%; Score 18.4; DB 7; Length 3180;
Best Local Similarity 95.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTCA 20
DB 1677 AGTGAGCCACCAAGTGTCCTCA 1658

RESULT 13
US-09-919-039-148/c
; Sequence 148, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR FILING DATE: 2002-09-09
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 148
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CBI
US-09-919-039-148

Query Match          92.0%; Score 18.4; DB 3; Length 3229;
Best Local Similarity 95.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTCA 20
DB 2794 AGTGAGCCACCAAGTGTCCTCA 2775

RESULT 14
US-10-208-408-22/c
; Sequence 22, Application US/10208408
; Publication No. US20030096272A1
; GENERAL INFORMATION:
; APPLICANT: Schebye, Xiao Min
; TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
; FILE REFERENCE: PA-0048-1 US
; CURRENT APPLICATION NUMBER: US/10/208,408
; CURRENT FILING DATE: 2002-07-29
; PRIOR FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030096272A1 1250434CBI
US-10-208-408-22

Query Match          92.0%; Score 18.4; DB 6; Length 3229;
Best Local Similarity 95.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTCA 20
DB 2794 AGTGAGCCACCAAGTGTCCTCA 2775

RESULT 15
US-10-084-817-113/c
; Sequence 113, Application US/10084817
; Publication No. US2003011909A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 113
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1250434CB1
US-10-084-817-113

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Query Match          92.0%; Score 18.4; DB 6; Length 3229;
Best Local Similarity 95.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AATGAGCCACCAGTGTCCAA 20
        |||||||||||||||
Db      2794 AGTGAGCCACCAGTGTCCAA 2775

```

Search completed: May 21, 2006, 21:48:58
Job time : 825 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:33:45 ; Search time 13.5 Seconds
(without alignments)
104.527 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtgtccaa 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_New:**

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq**
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq**
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq**
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq**
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq**
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq**
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq**
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.2	76.0	6327	7	US-11-217-529-75787 Sequence 75787, A
2	14.2	71.0	25	7	US-11-217-529-13735 Sequence 13735, A
3	14.2	71.0	163	7	US-11-301-554-1491 Sequence 1491, Ap
4	14.2	71.0	166	7	US-11-301-554-1393 Sequence 1393, Ap
5	14.2	71.0	166	7	US-11-301-554-1442 Sequence 1442, Ap
6	14.2	71.0	196	7	US-11-301-554-125 Sequence 125, App
7	14.2	71.0	422	7	US-11-301-554-1795 Sequence 1795, Ap
8	14.2	71.0	638	7	US-11-301-554-1283 Sequence 1283, Ap
9	14.2	71.0	663	7	US-11-217-529-710 Sequence 710, App
10	14.2	71.0	1041	7	US-11-301-924-21 Sequence 21, Appl
11	14.2	71.0	4600	7	US-11-301-554-1797 Sequence 1797, Ap
12	14.2	71.0	394191	6	US-10-506-549-3 Sequence 3, Appl
13	13.8	69.0	244	6	US-10-488-619-1090 Sequence 1090, Ap
14	13.8	69.0	2081	6	US-10-505-928-764 Sequence 764, App
15	13.8	69.0	3127	6	US-10-196-749-83 Sequence 83, Appl
16	13.8	69.0	17569	7	US-11-301-554-1804 Sequence 1804, Ap
17	13.6	68.0	192	7	US-11-217-529-174455 Sequence 174455, A
18	13.6	68.0	396	7	US-11-217-529-76998 Sequence 76998, A
19	13.6	68.0	438	7	US-11-217-529-78028 Sequence 78028, A
20	13.6	68.0	468	6	US-10-488-619-821 Sequence 821, App
21	13.6	68.0	711	7	US-11-217-529-4803 Sequence 4803, Ap
22	13.6	68.0	1446	7	US-11-217-529-76480 Sequence 76480, A
23	13.6	68.0	1506	7	US-11-217-529-81781 Sequence 81781, A
24	13.6	68.0	1749	7	US-11-217-529-2267 Sequence 2267, Ap
25	13.6	68.0	2379	7	US-11-217-529-79342 Sequence 79342, A

ALIGNMENTS

RESULT 1

US-11-217-529-75787
; Sequence 75787, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75787
; LENGTH: 6327
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75787

Query Match 76.0%; Score 15.2; DB 7; Length 6327;
Best Local Similarity 85.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AATGAGCCACCAGTGTCCAA 20

DB 2074 AAGGAGCTCCAGAGTCCAA 2093

RESULT 2

US-11-217-529-13735/c
; Sequence 13735, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13735
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-13735

Query Match 71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCA 19
DB 24 ACTGAGCCGCCAGTGTCCA 6

RESULT 3

US-11-301-554-1491
; Sequence 1491, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:

; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1491
; LENGTH: 163
; TYPE: DNA
; ORGANISM: Homo sapiens

US-11-301-554-1491

Query Match 71.0%; Score 14.2; DB 7; Length 163;

Best Local Similarity 84.2%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCA 19
DB 69 AACCTGCCACCAGTGTCCA 87

RESULT 4

US-11-301-554-1393/c
; Sequence 1393, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:

; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1393
; LENGTH: 166
; TYPE: DNA
; ORGANISM: Homo sapiens

US-11-301-554-1393

Query Match 71.0%; Score 14.2; DB 7; Length 166;
Best Local Similarity 84.2%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCA 19
DB 95 AACCTGCCACCAGTGTCCA 77

RESULT 5

US-11-301-554-1442
; Sequence 1442, Application US/11301554
; Publication No. US20060088527A1

GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; PRIOR FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1442
; LENGTH: 166
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1442

Query Match 71.0%; Score 14.2; DB 7; Length 166;
Best Local Similarity 84.2%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTCA 19
Db 72 AACCTGCCACCAAGTGTCCTCA 90

RESULT 6
US-11-301-554-125
; Sequence 125, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; PRIOR FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-125

Query Match 71.0%; Score 14.2; DB 7; Length 196;
Best Local Similarity 84.2%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTCA 19
Db 102 AACCTGCCACCAAGTGTCCTCA 120

RESULT 7
US-11-301-554-1795/c
; Sequence 1795, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: McNabb, Andria
; APPLICANT: Bangur, Chaitanya S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; PRIOR FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754

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; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 09/658,824
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1795
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 295, 378, 390
; OTHER INFORMATION: n = A,T,C or G
US-11-301-554-1795

Query Match      71.0%; Score 14.2; DB 7; Length 422;
Best Local Similarity 84.2%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 19
DB 130 AACCTGCCACCAGTGTCCTCA 112

RESULT 8
US-11-301-554-1283/c
; Sequence 1283, Application US/11301554
; Publication No. US2006098527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705

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; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1283
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1283

Query Match      71.0%; Score 14.2; DB 7; Length 638;
Best Local Similarity 84.2%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 19
DB 389 AACCTGCCACCAGTGTCCTCA 371

RESULT 9
US-11-217-529-710/c
; Sequence 710, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 710
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-710

Query Match      71.0%; Score 14.2; DB 7; Length 663;
Best Local Similarity 84.2%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 19
DB 316 ACTGAGCCGCCAGTGTCCTCA 298

RESULT 10
US-11-301-924-21
; Sequence 21, Application US/11301924
; Publication No. US20060090218A1
; GENERAL INFORMATION:
; APPLICANT: Joshua Z. Levin
; APPLICANT: Ken Phillips
; APPLICANT: Greg Budziszewski
; APPLICANT: Fred Meins
; APPLICANT: Zhenya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; FILE REFERENCE: 31481USNP
; CURRENT APPLICATION NUMBER: US/11/301,924
; CURRENT FILING DATE: 2005-12-13

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Query Match 71.0%; Score 14.2; DB 7; Length 1041;
Best Local Similarity 84.2%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
PRIOR APPLICATION NUMBER: US/09/896,186
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/222,202
PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-11-301-924-21

Query Match 71.0%; Score 14.2; DB 7; Length 1041;
Best Local Similarity 84.2%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCGA 19
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DB 49 AATGAGCCACCACTGTCCGA 67

RESULT 11

US-11-301-554-1797
Sequence 1797, Application US/11301554
Publication No. US20060088527A1

GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Kalos, Michael D.
APPLICANT: Sleath, Paul R.
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margarita
APPLICANT: Carter, Darick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.478C21
CURRENT APPLICATION NUMBER: US/11/301,554
CURRENT FILING DATE: 2005-12-13
PRIOR APPLICATION NUMBER: US 10/283,017
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US 10/113,872
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 10/017,754
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 09/902,941
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/849,626
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 09/736,457
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 09/702,705
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: US 09/677,419
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 09/671,325
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/658,824
PRIOR FILING DATE: 2000-09-08

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1797
LENGTH: 4600
TYPE: DNA
ORGANISM: Homo sapiens
US-11-301-554-1797

Query Match 71.0%; Score 14.2; DB 7; Length 4600;
Best Local Similarity 84.2%; Pred. No. 61;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATGAGCCACCACTGTCCCA 19
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DB 3767 AACTGCGCCACCACTGTCCCA 3785

RESULT 12

US-10-506-549-3/c
Sequence 3, Application US/10506549
Publication No. US20060100417A1
GENERAL INFORMATION:
APPLICANT: APPLERA CORPORATION
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001361-US
CURRENT APPLICATION NUMBER: US/10/506,549
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/361,343
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 394191
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(394191)
OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

Query Match 71.0%; Score 14.2; DB 6; Length 394191;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACCACTGTCCAA 20
|||
DB 130263 ATGAGCCACCACTGTCCAA 130245

RESULT 13

US-10-488-619-1090
Sequence 1090, Application US/10488619
Publication No. US20060099578A1
GENERAL INFORMATION:
APPLICANT: Greenlee, Winner and Sullivan, P.C.
TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
FILE REFERENCE: 98-01 WO
CURRENT APPLICATION NUMBER: US/10/488,619
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 3040
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1090
LENGTH: 244
TYPE: DNA
ORGANISM: Mus musculus
US-10-488-619-1090

Query Match 69.0%; Score 13.8; DB 6; Length 244;
Best Local Similarity 88.2%; Pred. No. 55;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGCCACCACTGTCCCA 19
|||
DB 95 TGAGCCACCACTGTCCCA 111

RESULT 14

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US-10-505-928-764
; Sequence 764, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 764
; LENGTH: 2081
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-764

Query Match      69.0%; Score 13.8; DB 6; Length 2081;
Best Local Similarity 88.2%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 TGAGCCACCAGTGTCCTCA 19
      ||||| ||||| |||||
Db      1596 TGAGCAACCATGTGTCCA 1612

RESULT 15
US-10-196-749-83/c
; Sequence 83, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 83
; LENGTH: 3127

; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-83

Query Match      69.0%; Score 13.8; DB 6; Length 3127;
Best Local Similarity 88.2%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GAGCCACCAGTGTCCTCA 20
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Db      1417 GTGCCACGAGTGTCCTCA 1401

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Job time : 14.5 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-10-766-185-4

Perfect score: 20

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2296392

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: gb_pr.*

6: gb_ro.*

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8: gb_ey.*

9: gb_un.*

10: gb_vi.*

11: gb_ov.*

12: gb_htg.*

13: gb_in.*

14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	49	2	BD187062
2	16	80.0	16	2	AX2927927
3	15.2	76.0	21	2	DD159257
4	14	70.0	49	2	BD187064
5	13.6	68.0	40	2	AR119846
6	13.6	68.0	40	2	AX077752
7	13.6	68.0	41	2	AR119858
8	13.6	68.0	41	2	AX077751
9	13.6	68.0	41	2	AX518106
10	13.6	68.0	42	2	AR119859
11	13.6	68.0	42	2	AX224363
12	13.4	67.0	20	2	AR312573
13	13.4	67.0	27	2	A25211
14	13.4	67.0	27	2	E09139
15	13	65.0	28	2	A24719
16	13	65.0	28	2	A24722
17	12.8	64.0	24	2	AR640085
18	12.8	64.0	24	2	AR640086

C	19	12.8	64.0	24	2	AX544252	Sequence
C	20	12.8	64.0	24	2	AX544253	Sequence
C	21	12.8	64.0	29	2	AR561068	Sequence
C	22	12.8	64.0	38	2	CO801003	Sequence
C	23	12.8	64.0	47	2	AR290208	Sequence
C	24	12.8	64.0	50	2	AR685481	Sequence
C	25	12.6	63.0	21	2	AR531344	Sequence
C	26	12.6	63.0	21	2	AX097369	Sequence
C	27	12.6	63.0	26	2	AR119845	Sequence
C	28	12.6	63.0	27	2	DD187294	Sequence
C	29	12.6	63.0	30	2	DD187291	Sequence
C	30	12.6	63.0	38	2	AR287012	Sequence
C	31	12.6	63.0	38	2	AR399002	Sequence
C	32	12.6	63.0	39	2	AR014283	Sequence
C	33	12.6	63.0	39	2	AR103038	Sequence
C	34	12.6	63.0	39	2	AR364199	Sequence
C	35	12.4	62.0	20	2	AR067326	Sequence
C	36	12.4	62.0	20	2	CS145074	Sequence
C	37	12.4	62.0	27	2	BD103613	Peptide a
C	38	12.4	62.0	27	2	BD103615	Peptide a
C	39	12.4	62.0	27	2	BD103617	Peptide a
C	40	12.4	62.0	27	2	BD103620	Peptide a
C	41	12.4	62.0	27	2	DD165976	Mutains o
C	42	12.4	62.0	27	2	DD165977	Mutains o
C	43	12.4	62.0	27	2	AR577077	Sequence
C	44	12.4	62.0	27	2	AR577079	Sequence
C	45	12.4	62.0	27	2	AR577081	Sequence

ALIGNMENTS

RESULT 1	BD187062	49 bp DNA linear	PAT 17-JUN-2003
LOCUS	BD187062	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.	
DEFINITION	BD187062	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.	
ACCESSION	BD187062	1 GI:31879262	
VERSION	BD187062	WO 02099104-A/22.	
KEYWORDS	BD187062	synthetic construct	
SOURCE	BD187062	other sequences; artificial sequences.	
ORGANISM	BD187062	1 (bases 1 to 49)	
REFERENCE	BD187062	Hiraoka, M., Kondo, S. and Harada, H.	
AUTHORS	BD187062	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it	
TITLE	BD187062	Patent: WO 02099104-A 22 12-DEC-2002;	
JOURNAL	BD187062	POLA CHEMICAL INDUSTRIES INC, MASAHIRO HIRAOKA, SHINAE KONDO, HIROSHI HARADA	
COMMENT	BD187062	OS Artificial Sequence	
	BD187062	PN WO 02099104-A/22	
	BD187062	PD 13-DEC-2002	
	BD187062	PF 04-JUN-2002	WO 2002JP005482
	BD187062	PR 05-JUN-2001	JP 01P 169948, 05-JUN-2001 JP 01P 169949 PI
	BD187062	MASAHIRO HIRAOKA, SHINAE KONDO, HIROSHI HARADA	
	BD187062	PC C12N15/09, C12Q1/68, C07K14/47, C07K19/00	
	BD187062	CC Description of Artificial Sequence: synthetic DNA FH Key	
	BD187062	Location/Qualifiers	
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	BD187062	source	1..49
	BD187062	/organism='synthetic construct'	
	BD187062	/mol_type='genomic DNA'	
	BD187062	/db_xref='taxon:32630'	
ORIGIN	BD187062		
Query Match	BD187062	100.0%; Score 20; DB 2; Length 49;	
Best Local Similarity	BD187062	100.0%; Pred. No. 17;	
Matches	BD187062	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	BD187062	1 GGAGCTAACATCTCCAAGTC 20	

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Db          26 GGAGCTAACATCTCCCAAGTC 45
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RESULT 2
AX927927
LOCUS      AX927927              16 bp  DNA      linear      PAT 19-DEC-2003
DEFINITION Sequence 13 from Patent WO03085110.
ACCESSION  AX927927
VERSION     AX927927.1  GI:40250734
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 16)
AUTHORS     Thru, C.A., h G.A.M. and Kristjansen, P.E.
TITLE       Oligomeric compounds for the modulation hif-1alpha expression
JOURNAL     Patent: WO 03085110-A 13 16-OCT-2003;
            Cureon A/S (DK)
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /notes="Description of Artificial Sequence:antisense
            oligonucleotide to human HIF-1a"
ORIGIN
Query Match      80.0%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4  GCTAACATCTCCCAAGT 19
        |||||
Db      1  GCTAACATCTCCCAAGT 16

RESULT 3
DD159257
LOCUS      DD159257              21 bp  DNA      linear      PAT 23-NOV-2005
DEFINITION Primer for detecting human enterobacteria.
ACCESSION  DD159257
VERSION     DD159257.1  GI:83957554
KEYWORDS    JP 2005124495-A/33.
SOURCE      unidentified
ORGANISM    unclassified sequences.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Watanabe, K., Fujimoto, J. and Matsuki, T.
TITLE       Primer for detecting human enterobacteria
JOURNAL     Patent: JP 2005124495-A 33 19-MAY-2005;
            KABUSHIKI KAISHA YAKULT HONSHA
COMMENT     OS Designed primer based on 16SrRNA of human enterobacteria PN
            JP 2005124495-A/33
            PD 19-MAY-2005
            PI koichi watanabe, junji fujimoto, takahiro matsuki CC
            FH Key Location/Qualifiers
FEATURES   Location/Qualifiers
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            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      76.0%; Score 15.2; DB 2; Length 21;
Best Local Similarity 85.0%; Pred. No. 5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GGAGCTAACATCTCCCAAGTC 20
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Db      2  GGAGCTTGCTTCTCCCAAGTC 21

Db          26 GGAGCTAACATCTCCCAAGTC 45
|||||
RESULT 4
BD187064
LOCUS      BD187064              49 bp  DNA      linear      PAT 17-JUN-2003
DEFINITION Polypeptide causing protein unstable in cell under aerobic
            condition and DNA encoding it.
ACCESSION  BD187064
VERSION     BD187064.1  GI:31879264
KEYWORDS    WO 02099104-A/24.
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 49)
AUTHORS     Hiraoka, M., Kondo, S. and Harada, H.
TITLE       Polypeptide causing protein unstable in cell under aerobic
            condition and DNA encoding it
JOURNAL     Patent: WO 02099104-A 24 12-DEC-2002;
            POLA CHEMICAL INDUSTRIES INC, MASAHIRO HIRAOKA, SHINAE KONDO, HIROSHI
            HARADA
COMMENT     OS Artificial Sequence
            PN WO 02099104-A/24
            PD 12-DEC-2002
            PF 04-JUN-2002 WO 2002JP005482
            PR 05-JUN-2001 JP 01P 169948, 05-JUN-2001 JP 01P 169949 PI
            MASAHIRO HIRAOKA, SHINAE KONDO, HIROSHI HARADA
            PC C12N15/09, C12Q1/68, C07K14/47, C07K19/00
            CC Description of Artificial Sequence: synthetic DNA FH Key
            PT source
            FT source
            Location/Qualifiers
            1..49
            /organism="Artificial Sequence".
FEATURES   Location/Qualifiers
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            1..49
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      70.0%; Score 14; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGAGCTAACATCTC 14
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Db      35 GGAGCTAACATCTC 48

RESULT 5
AR119846/c
LOCUS      AR119846              40 bp  DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 19 from patent US 6153421.
ACCESSION  AR119846
VERSION     AR119846.1  GI:14102545
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Yanagi, M., Bukh, J., Emerson, S.U. and Purcell, R.H.
TITLE       Cloned genomes of infectious hepatitis C viruses and uses thereof
JOURNAL     Patent: US 6153421-A 19 28-NOV-2000;
            Location/Qualifiers
FEATURES   Location/Qualifiers
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            /organism="unknown"
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ORIGIN
Query Match      68.0%; Score 13.6; DB 2; Length 40;
Best Local Similarity 80.0%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GGAGCTAACATCTCCAAGTC 20
        |||||
Db      33 GGAGCTAACCACTCCAGGCC 14

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RESULT 6
AX077752/c
LOCUS          40 bp      DNA      linear      PAT 22-FEB-2001
DEFINITION     Sequence 18 from Patent WO0106008.
ACCESSION      AX077752
VERSION        AX077752.1 GI:13157648
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Singh,S., Inamdar,A., Ullman,E.F., Cao,L. and Albagli,D.
TITLE          Multiplexed strand displacement for nucleic acid determinations
JOURNAL        Patent: WO 0106008-A 18 25-JAN-2001;
Aclara Biosciences, Inc. (US)
FEATURES       Location/Qualifiers
source         1..40
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="probe"
ORIGIN
Query Match   68.0%; Score 13.6; DB 2; Length 40;
Best Local Similarity 80.0%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGAGCTAACATCTCCCAAGTC 20
    ||| ||| ||| ||| ||| |||
Db 26 GGACCTCAGCTCTACAAGTC 7
    ||| ||| ||| ||| ||| |||
RESULT 7
AX119858
LOCUS          41 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION     Sequence 50 from patent US 6153421.
ACCESSION      AR119858
VERSION        AR119858.1 GI:14102557
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 41)
AUTHORS        Yanagi,M., Bukh,J., Emerson,S.U. and Purcell,R.H.
TITLE          Cloned genomes of infectious hepatitis C viruses and uses thereof
JOURNAL        Patent: US 6153421-A 50 28-NOV-2000;
Aclara Biosciences, Inc. (US)
FEATURES       Location/Qualifiers
source         1..41
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Query Match   68.0%; Score 13.6; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGAGCTAACATCTCCCAAGTC 20
    ||| ||| ||| ||| ||| |||
Db 8 GGAGCTAACATCTCCAGGCC 27
    ||| ||| ||| ||| ||| |||
RESULT 8
AX077751
LOCUS          41 bp      DNA      linear      PAT 22-FEB-2001
DEFINITION     Sequence 17 from Patent WO0106008.
ACCESSION      AX077751
VERSION        AX077751.1 GI:13157647
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Singh,S., Inamdar,A., Ullman,E.F., Cao,L. and Albagli,D.
TITLE          Multiplexed strand displacement for nucleic acid determinations
JOURNAL        Patent: WO 0106008-A 18 25-JAN-2001;
Aclara Biosciences, Inc. (US)
FEATURES       Location/Qualifiers
source         1..40
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="probe"
ORIGIN
Query Match   68.0%; Score 13.6; DB 2; Length 40;
Best Local Similarity 80.0%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGAGCTAACATCTCCCAAGTC 20
    ||| ||| ||| ||| ||| |||
Db 26 GGACCTCAGCTCTACAAGTC 7
    ||| ||| ||| ||| ||| |||
RESULT 9
AX518106/c
LOCUS          41 bp      DNA      linear      PAT 05-OCT-2002
DEFINITION     Sequence 4304 from Patent WO02052044.
ACCESSION      AX518106
VERSION        AX518106.1 GI:23567425
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE          Detection of genetic polymorphisms
JOURNAL        Patent: WO 02052044-A 4304 04-JUL-2002;
Riken (JP)
FEATURES       Location/Qualifiers
source         1..41
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
ORIGIN
Query Match   68.0%; Score 13.6; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGAGCTAACATCTCCCAAGTC 20
    ||| ||| ||| ||| ||| |||
Db 27 GAAGCTYAAGTCTCCAAGTC 8
    ||| ||| ||| ||| ||| |||
RESULT 10
AR119859
LOCUS          42 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION     Sequence 51 from patent US 6153421.
ACCESSION      AR119859
VERSION        AR119859.1 GI:14102558
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 42)
AUTHORS        Yanagi,M., Bukh,J., Emerson,S.U. and Purcell,R.H.
TITLE          Cloned genomes of infectious hepatitis C viruses and uses thereof
JOURNAL        Patent: US 6153421-A 51 28-NOV-2000;
Aclara Biosciences, Inc. (US)
FEATURES       Location/Qualifiers
source         1..42
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      68.0%; Score 13.6; DB 2; Length 42;
Best Local Similarity 80.0%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 8 GGAGCTAACCACTCCAGGCC 27

RESULT 11
AX224363
LOCUS AX224363 42 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 7 from Patent WO0161041.
ACCESSION AX224363
VERSION AX224363.1 GI:15554615
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Sharat,S., Cao,L., Hooper,H.H., Albagli,D., Anderson,R. and Zeng,S.
TITLE Multiple-site reaction device and method
JOURNAL Patent: WO 0161041-A 7 23-AUG-2001;
FEATURES
source 1..42
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/notes="probe"
misc_feature 41
note="n = triethyleneglycl"
misc_feature 42
note="n = biotinTEG"

ORIGIN
Query Match      68.0%; Score 13.6; DB 2; Length 42;
Best Local Similarity 80.0%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 15 GGACCTCAGCTTACAAAGTC 34

RESULT 12
AR312573
LOCUS AR312573 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3110 from patent US 6559294.
ACCESSION AR312573
VERSION AR312573.1 GI:31705999
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 3110 06-MAY-2003;
FEATURES
FRX;
Location/Qualifiers
source 1..20
/mol_type="unknown"
/organism="genomic DNA"

ORIGIN
Query Match      67.0%; Score 13.4; DB 2; Length 20;
Best Local Similarity 73.7%; Pred. No. 4.7e+04;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAAAGTC 20
Db 20 GAGCYRAGATCTCGAGGTC 2

RESULT 14
E09139/c
LOCUS E09139 27 bp DNA linear PAT 29-SBP-1997
DEFINITION Synthetic DNA for Alu specific primer.
ACCESSION E09139
VERSION E09139.1 GI:22025765
KEYWORDS JP 1995115999-A/2.
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Andoreasu,H.A. and Yan,P.
TITLE DETECTING METHOD FOR DNA ARRANGEMENT VARIATION
JOURNAL Patent: JP 1995115999-A 2 09-MAY-1995;
COMMENT INGENII BV
OS None
OC Artificial sequences.
PN JP 1995115999-A/2
PD 09-MAY-1995
PF 22-MAY-1992 JP 1992130668
PI ANDOREASU HERARUDOSU AITSUTERURINDEN, YAN FUEIKU PC
CC C12Q1/68,C12N15/00,G01N27/447,G01N27/447;
CC strandedness: Single;
CC topology: Linear;
CC key Location/Qualifiers
FH FT source 1..27
FT misc_feature 1..27
FT notes="Alu specific primer".
FEATURES
source Location/Qualifiers
1..27
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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ORIGIN

Query Match 67.0%; Score 13.4; DB 2; Length 27;
 Best Local Similarity 73.7%; Pred. No. 4.7e+04;
 Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAAAGTC 20
 ||||:|||||
 Db 20 GAGCTAACATCTCCAAAGTC 2

RESULT 15

A24719/c 28 bp DNA linear PAT 24-JAN-1995

LOCUS A24719

DEFINITION primer 2065.

ACCESSION A24719

VERSION A24719.1 GI:833452

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 28)

AUTHORS Little, S., Ferris, R.M. and Robertson, N.H.

TITLE Detection method for nucleotide sequences

JOURNAL Patent: EP 0497527-A 71 05-AUG-1992;

IMPERIAL CHEMICAL INDUSTRIES PLC; ZENECA LIMITED

FEATURES

Location/Qualifiers

1..28

source

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

ORIGIN

Query Match 65.0%; Score 13; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACATCTCCAAAGT 19
 |||||
 Db 27 AACATCTCCAAAGT 15

Search completed: May 21, 2006, 22:09:02

Job time : 1032.5 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:34:08 ; Search time 386 Seconds
(without alignments)
361.256 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggagctaacatctcccaagtc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5218926

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_8:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*
15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	20	100.0	20	13	ADQ88723	Adg88723 Human hyp
2	20	100.0	20	13	ADQ88724	Adg88724 Human HIF
3	20	100.0	49	8	ABZ76611	Abz76611 Human HIF
4	16	80.0	16	10	AAL56916	Aal56916 Human hyp
5	15.2	76.0	21	14	AEAL5801	Aeal5801 Human Ent
6	14.2	71.0	26	14	AEC27934	Aec27934 Human all
7	14.2	71.0	26	14	AEC25568	Aec25568 Human all
8	14.2	71.0	30	12	ADO31421	Ado31421 Human CFT
9	14	70.0	49	8	ABZ76613	Abz76613 Human HIF
C 10	13.8	69.0	25	9	ACIL1456	Acil1456 Human mic
11	13.8	69.0	36	14	AED66358	Aed66358 Recombina
12	13.8	69.0	36	14	ABZ66354	Abz66354 Recombina
13	13.8	69.0	41	6	ABZ23749	Abz23749 Human mem
14	13.8	69.0	41	6	ABZ23750	Abz23750 Human mem
C 15	13.6	68.0	27	12	ADO31172	Ado31172 Human ger
16	13.6	68.0	30	3	AAH76302	Aah76302 Mycobacte
C 17	13.6	68.0	40	2	AAx24853	Aax24853 Primer J4
18	13.6	68.0	40	5	AAF30251	Aaf30251 Dystrophi

ALIGNMENTS

RESULT 1
ADQ88723/c
ID ADQ88723 standard; DNA; 20 BP.

XX AC ADQ88723;

XX DT 21-OCT-2004 (first entry)

XX DE Human hypoxia inducible factor-1 gene fragment seqid 2.

XX KW RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity; cancer; infection; inflammation; tumour formation; ss.

XX OS Homo sapiens.

XX PN US2004152655-A1.

XX PD 05-AUG-2004.

XX PF 28-JAN-2004; 2004US-00766185.

XX PR 31-JAN-2003; 2003US-0444367P.

XX PA (YOON/) YOON H.

XX PA (MAOL/) MAO L.

XX PA (LEBY/) LEE Y B.

XX PA (AHNC/) AHN C.

XX PA (JTAN/) JIANG X.

XX PI Yoon H, Mao L, Lee YB, Ahn C, Jiang X;

XX DR WPI; 2004-561492/54.

XX PT New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), useful for inhibiting expression of HIF-1 and inducing cytotoxicity in several cancer cells.

XX PS Example 4; SEQ ID NO 3; 35pp; English.

XX CC The invention describes a compound, RX-0047 or RX-0149 targeted to a

Aaf30252 Dystrophi
Aax24837 Infectiou
Abz47520 Human Atp
Acc59493 Multiple
Aax24838 Infectiou
Aas11922 Duplex fo
Aax3784 PCR prime
Aaq33142 Inter-Alu
Adg87085 Light cha
Adg87088 Light cha
Adj78661 Pancreat
Adn27437 CFT gene
Ado50557 CFT inva
Ado31715 Human CFT
Aaf9782 Human gen
Aaq26890 Primer 20
Aaq26893 Primer 20
Aec49071 Antisense
Aec49165 Antisense
Abz97442 Human IL4
Abz30473 Human IL4
Adj59261 Oligonuel
Ado44751 Human oli
Adu40891 Knock-dow
Abt05788 Nod2 rela
Abt05789 Nod2 rela
Ado35304 Cardiomyo

C 19 13.6 68.0 40 5 AAF30252
20 13.6 68.0 41 2 AAX24837
C 21 13.6 68.0 41 6 ABZ47520
22 13.6 68.0 41 8 ACC59493
23 13.6 68.0 42 2 AAX24838
24 13.6 68.0 42 5 AAS11922
C 25 13.4 67.0 20 2 AAX3784
26 13.4 67.0 27 2 Aaq33142
27 13.4 67.0 29 10 Adg87085
28 13.4 67.0 47 10 Adg87088
C 29 13.2 66.0 21 7 Adj78661
30 13.2 66.0 28 12 Adn27437
31 13.2 66.0 28 12 Ado50557
32 13.2 66.0 28 12 Ado31715
C 33 13 65.0 21 4 AAF9782
34 13 65.0 28 2 Aaq26890
35 13 65.0 28 2 Aaq26893
36 12.8 64.0 18 14 AEC49071
37 12.8 64.0 18 14 AEC49165
C 38 12.8 64.0 20 10 ABZ97442
39 12.8 64.0 20 11 ABD30473
C 40 12.8 64.0 20 12 ADJ59261
C 41 12.8 64.0 20 12 ADO44751
C 42 12.8 64.0 21 13 ADU40891
C 43 12.8 64.0 24 6 ABT05788
C 44 12.8 64.0 24 6 ABT05789
45 12.8 64.0 26 12 ADO35304

CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
 CC where the oligonucleotide compound inhibits the expression of human HIF-
 CC 1. Also described are: a method of inhibiting the expression of HIF-1 in
 CC human cells or tissues; and a method of inducing cytotoxicity in a cancer
 CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a
 CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'
 CC atgagccaccagtgctca 3' and SEQ ID NO. 4, 5' ggagctaacatctccaagtc 3',
 CC respectively). The compounds are useful for inhibiting the expression of
 CC HIF-1 and inducing the cytotoxicity in several cancer cells. The
 CC antisense compounds are also useful for preventing or delaying infection,
 CC inflammation, or tumour formation. This sequence represents a site on the
 CC HIF-1 to which antisense oligonucleotides can be targeted in order to
 CC control HIF-1 gene expression.

XX SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
 DB 20 GGAGCTAACATCTCCAAGTC 1

RESULT 2
 ADQ88724
 ID ADQ88724 standard; DNA; 20 BP.
 XX
 AC ADQ88724;
 DT 21-OCT-2004 (first entry)
 XX Human HIF-1 antisense oligonucleotide RX-0149.
 DE
 XX RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;
 KW cancer; infection; inflammation; tumour formation; ss;
 KW antisense oligonucleotide; antisense technology.

XX OS Homo sapiens.
 XX US2004152655-A1.
 XX PD 05-AUG-2004.
 XX PF 28-JAN-2004; 2004US-00766185.
 XX PR 31-JAN-2003; 2003US-0444367P.

XX (YOON/) YOON H.
 PA (MAOL/) MAO L.
 PA (LEEV/) LEE Y B.
 PA (AHNG/) AHN C.
 PA (JIAN/) JIANG X.
 XX Yoon H, Mao L, Lee YB, Ahn C, Jiang X;
 PI WPI; 2004-561492/54.

XX New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a
 PT nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
 PT useful for inhibiting expression of HIF-1 and inducing cytotoxicity in
 PT several cancer cells.

XX Claim 6; SEQ ID NO 4; 35pp; English.

XX The invention describes a compound, RX-0047 or RX-0149 targeted to a
 CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
 CC where the oligonucleotide compound inhibits the expression of human HIF-
 CC 1. Also described are: a method of inhibiting the expression of HIF-1 in
 CC human cells or tissues; and a method of inducing cytotoxicity in a cancer
 CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a
 CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'

CC atagccaccagtgctca 3' and SEQ ID NO. 4, 5' ggagctaacatctccaagtc 3',
 CC respectively). The compounds are useful for inhibiting the expression of
 CC HIF-1 and inducing the cytotoxicity in several cancer cells. The
 CC antisense compounds are also useful for preventing or delaying infection,
 CC inflammation, or tumour formation. This sequence represents a human HIF-1
 CC antisense oligonucleotide.

XX SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
 DB 1 GGAGCTAACATCTCCAAGTC 20

RESULT 3
 ABZ76611
 ID ABZ76611 standard; DNA; 49 BP.
 XX
 AC ABZ76611;
 XX
 DT 30-APR-2003 (first entry)
 XX Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:24.

XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
 KW NLS; ODD; PCR primer; ss.

XX OS Homo sapiens.

XX WO200299104-A1.

XX PD 12-DEC-2002.

XX 04-JUN-2002; 2002WO-JP005482.

XX 05-JUN-2001; 2001JP-00169948.

XX 05-JUN-2001; 2001JP-00169949.

XX (POK) POLA CHEM IND INC.

XX (HIEA/) HIRAOKA M.

XX (KOND/) KONDOSH S.

XX Hiraoka M, Kondoh S, Harada H;

XX WPI; 2003-148670/14.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic
 PT conditions to proteins within the cell, useful for treatment of cancer
 PT and improvement of microbial fermentation.

XX Example; Page 24; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDEMLAPYIPMDDFQL
 CC see ABP57669) (I), or encoding a fusion protein containing at least 16
 CC residues of (I), a nuclear localisation signal (NLS), and another
 CC protein, and imparting relative stability under specific conditions of
 CC oxygen concentration within the cell. Also described: (1) vectors
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing
 CC the fusion protein by culture of the transformed cells; (4) detecting
 CC hypoxic conditions in cells by monitoring the stability of the protein
 CC fused to (I) in cells transformed by vectors containing the DNA; (5)
 CC regulating the stability of proteins within the cell by transformation
 CC with the DNA; (6) inhibiting the development of cells under hypoxic
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
 CC tension. (I) has cytostatic activity, and can be used for the

CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
 CC solid tumour, and in gene therapy, (1) can be used in industrial
 CC microbial fermentation, and in medicine, especially in the treatment of
 CC tumours containing hypoxic regions. The present sequence represents a PCR
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)
 CC domain, which is used in an example from the present invention
 XX
 SQ Sequence 49 BP; 15 A; 11 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 49;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20

DB 26 GGAGCTAACATCTCCAAAGTC 45

RESULT 4

AAL56916

ID AAL56916 standard; DNA; 16 BP.

XX

AC AAL56916;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human hypoxia-inducible factor-1 alpha antisense oligo #12.

XX

KW HIF-1alpha; hypoxia-inducible factor-1 alpha; human; antisense; cancer;

KW pre-eclampsia; cytostatic; gynaecological; antiinflammatory; neutropic;

KW neuroprotective; ss.

XX

OS Homo sapiens.

XX

PN WO2003085110-A2.

XX

PD 16-OCT-2003.

XX

PF 04-APR-2003; 2003WO-IB001758.

XX

PR 05-APR-2002; 2002US-0370126P.

XX

PA (CURE-) CUREON AS.

XX

PI Thru CA, Hog AM, Kristjansen PEG;

XX

DR WPI; 2003-812728/76.

XX

XX New oligonucleotide that modulates hypoxia-inducible factor-1alpha,

PT useful for treating e.g. cancer or Alzheimer's disease.

XX

PS Claim 1; Page 41; Opp; English.

XX

CC The present invention relates to compounds capable of modulating hypoxia-

CC inducible factor-1alpha (HIF1a). The compounds are used to treat patients

CC with, or at risk of developing, cancer (e.g. of breast, prostate,

CC pancreas, lung), pre-eclampsia, inflammatory bowel disease or Alzheimer's

CC disease, for modulating angiogenesis, proliferation of erythrocytes and

CC other cells, iron, glucose and energy metabolism, pH regulation, tissue

CC invasion, apoptosis, multiple drug resistance, cellular stress responses,

CC and matrix metabolism, especially apoptosis where modulation is

CC sensitivity to an apoptotic stimulus, particularly a chemotherapeutic

CC agent and for inhibiting proliferation of cells (especially cancer cells)

CC in vitro. The present sequence is an antisense oligonucleotide against

CC HIF1alpha identified in the exemplification of the invention

XX

SQ Sequence 16 BP; 5 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

XX

Query Match 80.0%; Score 16; DB 10; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAAGT 19

DB 1 GCTAACATCTCCAAAGT 16

RESULT 5

AEA15801

ID AEA15801 standard; DNA; 21 BP.

XX

AC AEA15801;

XX

DT 28-JUL-2005 (first entry)

XX

DE Human Enterobacterium detection-related PCR primer SeqID33.

XX

KW microorganism detection; microorganism identification; DNA detection;

KW DNA amplification; enterobacteriaceae infection; antibacterial; PCR;

KW primer; ss.

XX

OS Bacteria.

XX

PN JP2005124495-A.

XX

PD 19-MAY-2005.

XX

PF 24-OCT-2003; 2003JP-00364188.

XX

PR 24-OCT-2003; 2003JP-00364188.

XX

PA (HONS) YAKULT HONSHA KK.

XX

DR WPI; 2005-359465/37.

XX

XX Novel primer comprising specific nucleotide sequences, useful for

PT detection and identification of human Enterobacterium such as Clostridium

PT butyricum.

XX

PS Claim 1; SEQ ID NO 33; 20pp; Japanese.

XX

XX This invention relates to a novel PCR primer for detecting human

CC Enterobacterium, comprising one of 39 fully defined 18-26 nucleotide

CC sequences (SEQ ID No. 1-39) given in the specification or a sequence

CC complementary to the above mentioned base sequence. The invention enables

CC rapid and convenient detection and identification of human

CC Enterobacterium. The present sequence is that of a PCR primer which was

CC used for detecting human Enterobacterium in the method of the invention.

XX

SQ Sequence 21 BP; 4 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

XX

Query Match 76.0%; Score 15.2; DB 14; Length 21;

Best Local Similarity 85.0%; Pred. No. 8.2e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20

DB 2 GGAGCTTGCTTCTCCAAAGTC 21

XX

RESULT 6

AEC27934

ID AEC27934 standard; DNA; 26 BP.

XX

AC AEC27934;

XX

DT 17-NOV-2005 (first entry)

XX

DE Human allele-specific oligonucleotide #3954.

XX

KW Haplotype mapping; genetic marker; single nucleotide polymorphism; SNP;

KW major histocompatibility complex; MHC; HLA; human leukocyte antigen;

KW immune disorder; inflammation; inflammatory bowel disease;

KW ulcerative colitis; Crohn's disease; rheumatoid arthritis; diabetes;

KW diabetes mellitus; myasthenia gravis; vitiligo; Graves disease;

KW Hashimoto's disease; Addison's disease; gastritis; autoimmune hepatitis;

KW rheumatism; systemic lupus erythematosus; scleroderma; polymyositis;
 KW dermatomyositis; pernicious anemia; primary biliary cirrhosis;
 KW idiopathic thrombocytopenia purpura; Sjogrens syndrome;
 KW multiple sclerosis; Reiter's syndrome; psoriasis; antiinflammatory;
 KW gastrointestinal-gen.; antitumor; immunomodulator; immunosuppressive;
 KW antirheumatic; antidiabetic; muscular-gen.;
 KW neuroprotective; dermatological; antithyroid; hepatotropic; antianemic;
 KW SNP detection.
 KW SNP detection.
 OS Homo sapiens.
 XX WO2005082110-A2.
 XX 09-SEP-2005.
 XX 28-FEB-2005; 2005WO-US006628.
 XX 26-FEB-2004; 2004US-0547823P.
 XX (ILLU-) ILLUMINA INC.
 XX Oliphant A, Murray S;
 XX WPI; 2005-638856/65.
 XX Identifying single nucleotide polymorphism (SNP) haplotype that
 XX correlates with the HLA type, useful for diagnosing an immunological or
 XX inflammatory condition, comprises providing SNPs in the major
 XX histocompatibility complex region.
 XX Example 1; SEQ ID NO 3954; 175pp; English.
 XX The invention relates to a method of identifying the nucleotide for each
 XX of a set of single nucleotide polymorphisms (SNPs) in the major
 XX histocompatibility complex (MHC) region in a population of individuals,
 XX comprising providing the HLA type for the individuals and identifying an
 XX SNP haplotype in the population that correlates with the HLA type, where
 XX the SNP haplotype comprises the SNPs in the MHC region. The invention
 XX also relates to a method of predicting the HLA type of an individual, a
 XX method of determining the presence or absence of an allelic variant of an
 XX MHC gene in an individual, a method of identifying an SNP haplotype that
 XX correlates with susceptibility to a disease or condition, and a method of
 XX determining the susceptibility of an individual to a disease or
 XX condition. The disease or condition is an immune disorder or inflammatory
 XX condition selected from inflammatory bowel disease, ulcerative colitis,
 XX Crohn's disease, rheumatoid arthritis, diabetes, diabetes mellitus,
 XX myasthenia gravis, vitiligo, Graves disease, Hashimoto's disease,
 XX Addison's disease, gastritis, autoimmune hepatitis, rheumatism, systemic
 XX lupus erythematosus, systemic sclerosis, polymyositis, dermatomyositis,
 XX pernicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia
 XX purpura, Sjogren's syndrome, multiple sclerosis, Reiter's syndrome and
 XX psoriasis. This sequence represents a human allele-specific
 XX oligonucleotide used in the scope of the invention.
 XX Sequence 26 BP; 5 A; 7 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 14; Length 26;
 Best Local Similarity 84.2%; Pred. No. 2.7e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCCAAGTC 20
 DB 5 GACCTAACATCTCCCAAGTC 23

RESULT 7
 AEC25568
 ID AEC25568 standard; DNA; 26 BP.
 XX AEC25568;
 XX 17-NOV-2005 (first entry)

XX Human allele-specific oligonucleotide #1588.
 DE Haplotype mapping; Genetic marker; single nucleotide polymorphism; SNP;
 XX major histocompatibility complex; MHC; HLA; human leukocyte antigen;
 KW immune disorder; inflammation; inflammatory bowel disease;
 KW ulcerative colitis; Crohns disease; rheumatoid arthritis; diabetes;
 KW diabetes mellitus; myasthenia gravis; vitiligo; Graves disease;
 KW Hashimoto's disease; Addison's disease; gastritis; autoimmune hepatitis;
 KW rheumatism; systemic lupus erythematosus; scleroderma; polymyositis;
 KW dermatomyositis; pernicious anemia; primary biliary cirrhosis;
 KW idiopathic thrombocytopenia purpura; Sjogrens syndrome;
 KW multiple sclerosis; Reiter's syndrome; psoriasis; antiinflammatory;
 KW gastrointestinal-gen.; antitumor; immunomodulator; immunosuppressive;
 KW antirheumatic; antidiabetic; muscular-gen.;
 KW neuroprotective; dermatological; antithyroid; hepatotropic; antianemic;
 KW SNP detection.
 OS Homo sapiens.
 XX WO2005082110-A2.
 XX 09-SEP-2005.
 XX 28-FEB-2005; 2005WO-US006628.
 XX 26-FEB-2004; 2004US-0547823P.
 XX (ILLU-) ILLUMINA INC.
 XX Oliphant A, Murray S;
 XX WPI; 2005-638856/65.
 XX Identifying single nucleotide polymorphism (SNP) haplotype that
 XX correlates with the HLA type, useful for diagnosing an immunological or
 XX inflammatory condition, comprises providing SNPs in the major
 XX histocompatibility complex region.
 XX Example 1; SEQ ID NO 1588; 175pp; English.

XX The invention relates to a method of identifying the nucleotide for each
 XX of a set of single nucleotide polymorphisms (SNPs) in the major
 XX histocompatibility complex (MHC) region in a population of individuals,
 XX comprising providing the HLA type for the individuals and identifying an
 XX SNP haplotype in the population that correlates with the HLA type, where
 XX the SNP haplotype comprises the SNPs in the MHC region. The invention
 XX also relates to a method of predicting the HLA type of an individual, a
 XX method of determining the presence or absence of an allelic variant of an
 XX MHC gene in an individual, a method of identifying an SNP haplotype that
 XX correlates with susceptibility to a disease or condition, and a method of
 XX determining the susceptibility of an individual to a disease or
 XX condition. The disease or condition is an immune disorder or inflammatory
 XX condition selected from inflammatory bowel disease, ulcerative colitis,
 XX Crohn's disease, rheumatoid arthritis, diabetes, diabetes mellitus,
 XX myasthenia gravis, vitiligo, Graves disease, Hashimoto's disease,
 XX Addison's disease, gastritis, autoimmune hepatitis, rheumatism, systemic
 XX lupus erythematosus, systemic sclerosis, polymyositis, dermatomyositis,
 XX pernicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia
 XX purpura, Sjogren's syndrome, multiple sclerosis, Reiter's syndrome and
 XX psoriasis. This sequence represents a human allele-specific
 XX oligonucleotide used in the scope of the invention.

Sequence 26 BP; 6 A; 7 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 14; Length 26;
 Best Local Similarity 84.2%; Pred. No. 2.7e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCCAAGTC 20
 DB 5 GACCTAACATCTCCCAAGTC 23

RESULT 8
 ID ADO31421 standard; DNA; 30 BP.
 AC ADO31421;
 XX
 XX
 DT 26-AUG-2004 (first entry)
 DE Human CFTR gene mutant probe for variant 1717-1G>A #2.
 XX
 XX Human; CFTR gene; ss; probe; cystic fibrosis;
 KW Cystic Fibrosis Transmembrane Conductance Regulator;
 KW invasive cleavage structure assay; INVADER; FRET;
 KW fluorescent resonance energy transfer; multiplexed amplification.
 XX
 XX Homo sapiens.
 XX WO2004046688-A2.
 XX
 XX 03-JUN-2004.
 XX
 XX 14-NOV-2003; 2003WO-US036611.
 XX
 XX 14-NOV-2002; 2002US-0426144P.
 PR 21-FEB-2003; 2003US-00371913.
 PR 26-JUN-2003; 2003US-00606577.
 PR 21-JUL-2003; 2003US-0489095P.
 PR 25-AUG-2003; 2003US-0497644P.
 PR 28-OCT-2003; 2003US-0515175P.
 PR 14-NOV-2003; 2003US-00713653.
 XX
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
 XX
 XX Accola M, Wigdal SS, Mast AL, Bartholomay CT, Kwiatkowski RW;
 PI Tevere V, Ip HS, Carroll K, Peterson P, Agarwal P, Jarvis N;
 PI Hall JG, Heisler L;
 XX
 XX WPI; 2004-420702/39.
 XX
 XX Detecting Cystic Fibrosis Transmembrane Conductance Regulator (CFTR)
 PT alleles, useful for screening mutations associated with cystic fibrosis,
 PT comprises exposing amplified CFTR target nucleic acid to detection
 PT assays.
 XX
 XX Example 7; SEQ ID NO 52; 147pp; English.
 PS
 XX The invention relates to detecting Cystic Fibrosis Transmembrane
 CC Conductance Regulator (CFTR) alleles comprising providing a sample
 CC comprising a CFTR target nucleic acid, amplifying the CFTR target
 CC acid with 25 cycles or fewer of a PCR to generate amplified target
 CC nucleic acid, and exposing the amplified target nucleic acid to detection
 CC assays configured to detect CFTR alleles under conditions such that the
 CC presence or absence of the CFTR alleles is detected, using an invasive
 CC cleavage structure assay (designated INVADER), employing FRET probes
 CC (fluorescent resonance energy transfer). Also included is a kit
 CC comprising a non-amplified oligonucleotide detection assay configured for
 CC detecting at least one CFTR allele or oligonucleotide detection assays
 CC configured for detecting a set of CFTR alleles where the set is a first
 CC set comprising 2789+5G to A, R1162X, R560T, 1898+1 G to A, del1507,
 CC N148T, and A455S, a second set comprising 3120+1G to A, 3659delC, G551D,
 CC N1303K, 1078delT, R334W, 711+1G to T, and 3849+10kb, a third set
 CC comprising 621+1G to T, W1282X, 1717-1G to A, and R117H, or a fourth set
 CC comprising R347P, G85E, G542X and R553X, or a fifth set comprising
 CC 2184delA. The non-amplified oligonucleotide detection assay or the
 CC oligonucleotide detection assays comprises first and second
 CC oligonucleotides configured to form an invasive cleavage structure in
 CC combination with a target sequence comprising the CFTR allele. The first
 CC oligonucleotide comprises a 5' portion and a 3' portion, where the 3'
 CC portion is configured to hybridise to the target sequence and the 5'
 CC portion is configured to not hybridise to the target sequence. The second
 CC oligonucleotide comprises a 5' portion and a 3' portion, where the 5'

CC portion is configured to hybridise to the target sequence and the 3'
 CC portion is configured to not hybridise to the target sequence. The method
 CC and kit are useful for detecting CFTR alleles, more particularly for
 CC screening nucleic acid samples e.g. from patients, for the presence of
 CC any one of a collection of mutations in the CFTR gene associated with
 CC cystic fibrosis. The method and compositions are useful for generating
 CC and analysing limited cycle, multiplexed amplification of a large
 CC collection of CFTR loci. The present sequence comprises a probe for the
 CC method of the invention detecting the mutant CFTR allele.

SQ Sequence 30 BP; 9 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 12; Length 30;
 Best Local Similarity 84.3%; Pred. No. 2.8e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGT 19
 |||||
 DB 9 GGAGAGACATCTCCCAAGT 27

RESULT 9

ABZ76613
 ID ABZ76613 standard; DNA; 49 BP.

XX
 AC ABZ76613;

XX
 DT 30-APR-2003 (first entry)

XX
 DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:26.

XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
 KW NLS; ODD; PCR primer; ss.

XX Homo sapiens.

XX WO200299104-A1.

XX 12-DEC-2002.

XX 04-JUN-2002; 2002WO-JP005482.

XX 05-JUN-2001; 2001JP-00169948.

XX 05-JUN-2001; 2001JP-00169949.

XX (POKK) POLA CHEM IND INC.

XX (HIRA/) HIRAOKA M.

XX (KOND/) KONDOH S.

XX Hiraoka M, Kondoh S, Harada H;

XX WPI; 2003-148670/14.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic
 PT conditions to proteins within the cell, useful for treatment of cancer
 PT and improvement of microbial fermentation.

XX Example; Page 24; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPVPMDDDFOL
 CC see AB957669) (I), or encoding a fusion protein containing at least 16
 CC residues of (I), a nuclear localisation signal (NLS), and another
 CC protein, and imparting relative stability under specific conditions of
 CC oxygen concentration within the cell. Also described: (1) vectors
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing
 CC the fusion protein by culture of the transformed cells; (4) detecting
 CC hypoxic conditions in cells by monitoring the stability of the protein
 CC fused to (I) in cells transformed by vectors containing the DNA; (5)
 CC regulating the stability of proteins within the cell by transformation
 CC with the DNA; (6) inhibiting the development of cells under hypoxic

CC conditions, using the fusion protein; (7) fusion proteins encoded by the
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
 CC tension. (i) has cytostatic activity, and can be used for the
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
 CC solid tumour, and in gene therapy. (i) can be used in industrial
 CC microbial fermentation, and in medicine, especially in the treatment of
 CC tumours containing hypoxic regions. The present sequence represents a PCR
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)
 CC domain, which is used in an example from the present invention
 XX
 SQ Sequence 49 BP; 15 A; 10 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 8; Length 49;
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTC 14
 |||||
 Db 35 GGAGCTAACATCTC 48

RESULT 10

AC111456/c
 ID AC111456 standard; DNA; 25 BP.

XX AC111456;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 11447.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 11447; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX

SQ Sequence 25 BP; 7 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;
 Best Local Similarity 88.2%; Pred. No. 4.4e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGTC 20
 |||||
 Db 20 GCGACATCTGCAAGTC 4

RESULT 11

AED66358

ID AED66358 standard; DNA; 36 BP.

XX AED66358;

XX 29-DEC-2005 (first entry)

DE Recombinant cytochrome P450 related P4503A4-Hsp70 sequence N.

XX expression; cytochrome P450; heat shock protein; protein synthesis;
 KW protein folding; gene expression; Hsp70; ds.

XX Unidentified.

XX KR2005028279-A.

XX 22-MAR-2005.

XX 18-SEP-2003; 2003KR-00065447.

XX 18-SEP-2003; 2003KR-00065447.

XX (AHNT/) AHN T H.

XX Ahn TH, Yang SY;

XX WPI; 2005-579519/59.

XX Method for increasing protein expression and catalytic activity of
 PT recombinant cytochrome p450 enzymes by co-expression with genes encoding
 PT heat shock proteins which function as molecular chaperone.

XX Disclosure; Page 3; 8pp; Korean.

XX The invention relates to a method for increasing protein expression and
 CC catalytic activity of recombinant cytochrome P450 enzymes by co-
 CC expression with genes encoding heat shock proteins (HSPs), where the heat
 CC shock proteins function as a molecular chaperone that regulate other
 CC protein synthesis and translocation, protein folding, gene expression,
 CC protein hydrolysis, protein aggregation, etc., so that the heat shock
 CC proteins induce increased protein expression and catalytic activity of
 CC recombinant cytochrome P450 enzymes. The method for increasing protein
 CC expression and catalytic activity of recombinant cytochrome P450 enzymes
 CC comprises co-expression of the recombinant cytochrome P450 enzyme genes
 CC with genes encoding heat shock proteins Hsp70 and HDJ-1, wherein the
 CC recombinant cytochrome P450 enzyme genes and the heat shock protein genes
 CC are isolated from human or rat; the recombinant cytochrome P450 enzyme
 CC genes and the heat shock protein genes are contained in one open reading
 CC frame; and the heat shock proteins induce increased amount and catalytic
 CC activity of the recombinant cytochrome P450 enzymes. This sequence
 CC represents DNA relating to the present invention.

XX Sequence 36 BP; 10 A; 10 C; 13 G; 3 T; 0 U; 0 Other;

```
Query Match          69.0%; Score 13.8; DB 14; Length 36;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAA 17
DB 12 GGAGCTAACATGCCAA 28

RESULT 12
AED66354
ID AED66354 standard; DNA; 36 BP.
XX
AC AED66354;
XX
DT 29-DEC-2005 (first entry)
XX
DE Recombinant cytochrome P450 related P450IA2-Hsp70 sequence N.
XX
KW expression; cytochrome P450; heat shock protein; protein synthesis;
KW protein folding; gene expression; Hsp70; ds.
XX
OS Unidentified.
XX
FN KR2005028279-A.
XX
PD 22-MAR-2005.
XX
PF 18-SEP-2003; 2003KR-00065447.
XX
PR 18-SEP-2003; 2003KR-00065447.
XX
PA (AHNT/) AHN T H.
XX
PI Ahn TH, Yang SY;
XX
DR WPI; 2005-579519/59.
XX
PT Method for increasing protein expression and catalytic activity of
PT recombinant cytochrome P450 enzymes by co-expression with genes encoding
PT heat shock proteins which function as molecular chaperone.
XX
PS Disclosure; Page 2; 8pp; Korean.
XX
CC The invention relates to a method for increasing protein expression and
CC catalytic activity of recombinant cytochrome P450 enzymes by co-
CC expression with genes encoding heat shock proteins (HSPs), where the heat
CC shock proteins function as a molecular chaperone that regulate other
CC protein synthesis and translocation, protein folding, gene expression,
CC protein hydrolysis, protein aggregation, etc., so that the heat shock
CC proteins induce increased protein expression and catalytic activity of
CC recombinant cytochrome P450 enzymes. The method for increasing protein
CC expression and catalytic activity of recombinant cytochrome P450 enzymes
CC comprises co-expression of the recombinant cytochrome P450 enzyme genes
CC with genes encoding heat shock proteins Hsp70 and HDJ-1, wherein the
CC recombinant cytochrome P450 enzyme genes and the heat shock protein genes
CC are isolated from human or rat; the recombinant cytochrome P450 enzyme
CC genes and the heat shock protein genes are contained in one open reading
CC frame; and the heat shock proteins induce increased amount and catalytic
CC activity of the recombinant cytochrome P450 enzymes. This sequence
CC represents DNA relating to the present invention.
XX
SQ Sequence 36 BP; 11 A; 11 C; 10 G; 4 T; 0 U; 0 Other;

Query Match          69.0%; Score 13.8; DB 14; Length 36;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAA 17
DB 13 GGAGCTAACATGCCAA 29

RESULT 13
ABZ23749
ID ABZ23749 standard; DNA; 41 BP.
XX
AC ABZ23749;
XX
DT 26-MAR-2003 (first entry)
XX
DE Human membrane vacuole transportation related protein 10.23 probe 1.
XX
KW Human; membrane vacuole transportation protein; 10.23; malignant tumour;
KW haemopathy; human immunodeficiency virus; HIV; immunological disease;
KW inflammation; probe; ss.
XX
OS Homo sapiens.
XX
PN CN1345830-A.
XX
PD 24-APR-2002.
XX
PF 29-SEP-2000; 2000CN-00125514.
XX
PR 29-SEP-2000; 2000CN-00125514.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-584316/63.
XX
PT A novel human membrane vacuole transportation related protein 10.23
PT polypeptide, useful for curing several diseases e.g. malignant tumor,
PT hemopathy, HIV infection, immunological disease and various inflammations
PT and epilepsy.
XX
PS Example 6; Page 19 (disclosure); 33pp; Chinese.
XX
CC The invention relates to a human membrane vacuole transportation related
CC protein 10.23. Also disclosed are the polynucleotide encoding the
CC polypeptide, and a method for preparing the polypeptide using DNA
CC recombination techniques. The polypeptide is useful for curing several
CC diseases including, malignant tumours, haemopathy, human immunodeficiency
CC virus (HIV) infection, immunological disease and various inflammations.
CC The current sequence represents a human membrane vacuole transportation
CC related protein 10.23 related probe sequence
XX
SQ Sequence 41 BP; 9 A; 15 C; 11 G; 6 T; 0 U; 0 Other;

Query Match          69.0%; Score 13.8; DB 6; Length 41;
Best Local Similarity 88.2%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAACTC 20
DB 23 GCTAACATCTCCAACTC 39

RESULT 14
ABZ23750
ID ABZ23750 standard; DNA; 41 BP.
XX
AC ABZ23750;
XX
DT 26-MAR-2003 (first entry)
XX
DE Human membrane vacuole transportation related protein 10.23 probe 2.
XX
KW Human; membrane vacuole transportation protein; 10.23; malignant tumour;
KW haemopathy; human immunodeficiency virus; HIV; immunological disease;
KW inflammation; probe; ss.
XX
OS Homo sapiens.
```

XX CN1345830-A.
 XX PD 24-APR-2002.
 XX PP 29-SEP-2000; 2000CN-00125514.
 XX PR 29-SEP-2000; 2000CN-00125514.
 XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX PI Mao Y, Xie Y;
 XX WI 2002-584316/63.
 XX A novel human membrane vacuole transportation related protein 10.23 polypeptide, useful for curing several diseases e.g. malignant tumor, hemopathy, HIV infection, immunological disease and various inflammations and epilepsy.
 XX Example 6; Page 19 (disclosure); 33pp; Chinese.
 XX The invention relates to a human membrane vacuole transportation related protein 10.23. Also disclosed are the polynucleotide encoding the polypeptide, and a method for preparing the polypeptide using DNA recombination techniques. The polypeptide is useful for curing several diseases including, malignant tumors, haemopathy, human immunodeficiency virus (HIV) infection, immunological disease and various inflammations. The current sequence represents a human membrane vacuole transportation related protein 10.23 related probe sequence
 XX Sequence 41 BP; 9 A; 15 C; 11 G; 6 T; 0 U; 0 Other;
 Query Match 69.0%; Score 13.8; DB 6; Length 41;
 Best Local Similarity 88.2%; Pred. No. 4.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GCTAACATCTCCCAAGTC 20
 DB 23 GGTACAGCTCCCAAGTC 39
 RESULT 15
 ADO31172/c
 ID ADO31172 standard; DNA; 27 BP.
 XX AC ADO31172;
 XX DT 12-AUG-2004 (first entry)
 XX DE Human germinal center associated nuclear protein gene primer #26.
 XX KW ss; primer; virucide; viral antigen inhibitor; transgenic;
 KW germinal center associated nuclear protein; GAMP; antibody;
 KW virus infection; human immunodeficiency virus; hepatitis C virus.
 XX OS Homo sapiens.
 XX WO2004040971-A1.
 XX PD 21-MAY-2004.
 XX PF 07-NOV-2003; 2003WO-JP014221.
 XX PR 07-NOV-2002; 2002WO-JP011598.
 XX PA (IMMU-) IMMUNOKICK INC.
 XX PI Sakaguchi N;
 XX WI 2004-411378/38.
 XX PT Transgenic mammal transformed with germinal center associated nuclear

PT protein (GAMP) gene for production of high-affinity antibodies as diagnostic reagents and disease therapy.
 XX Example 10; SEQ ID NO 30; 214pp; Japanese.
 XX The invention relates to transgenic non-human animals and their offspring which are transformed with germinal center associated nuclear protein (GAMP) gene. The GAMP gene, encoded protein and transgenic animals express GAMP can be used for the production of high-affinity antibodies to viral antigens for treatment and prevention of infection by viruses such as human immunodeficiency virus and hepatitis C virus. This sequence corresponds to a PCR primer to amplify a the human GAMP gene.
 XX Sequence 27 BP; 6 A; 4 C; 8 G; 9 T; 0 U; 0 Other;
 Query Match 68.0%; Score 13.6; DB 12; Length 27;
 Best Local Similarity 80.0%; Pred. No. 5.6e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GGAGCTAACATCTCCCAAGTC 20
 DB 23 GGTGAACATCTACCAAGTC 4
 Search completed: May 21, 2006, 22:31:22
 Job time : 390 secs

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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:49:17 ; Search time 2196 Seconds
(without alignments)
509.284 Million cell updates/sec

Title: US-10-766-185-4
Perfect score: 20
Sequence: 1 ggaagctaacatctccaagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 194034

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_est7:*
- 7: gb_est8:*
- 8: gb_est9:*
- 9: gb_est10:*
- 10: gb_est11:*
- 11: gb_est12:*
- 12: gb_est13:*
- 13: gb_est14:*
- 14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	72.0	26	11	AZ352012
2	14.2	71.0	47	11	AZ860255
3	13.8	69.0	49	1	A1348359
4	13.4	67.0	50	4	CA795439
5	13.2	66.0	47	11	AZ362217
6	13.2	66.0	47	14	CT391862
7	13.2	66.0	49	12	CC88587
8	13.2	66.0	50	11	AZ774523
9	12.8	64.0	32	13	CZ918458
10	12.8	64.0	41	11	AZ357818
11	12.6	63.0	28	12	CT795628
12	12.4	62.0	34	1	AI194779
13	12.2	61.0	28	13	CZ917814
14	12.2	61.0	35	11	BZ381186
15	12.2	61.0	37	11	AZ989635
16	12.2	61.0	46	14	AL946937
17	12.2	61.0	48	8	CV191608
18	12	60.0	33	14	AJ529162
19	12	60.0	33	14	ATH529282

C	20	12	60.0	41	14	AG191947
C	21	11.8	59.0	29	1	AM111394
C	22	11.8	59.0	36	11	AZ785517
C	23	11.8	59.0	43	1	AA908443
C	24	11.6	58.0	31	11	AZ473316
C	25	11.6	58.0	32	11	AZ806107
C	26	11.6	58.0	36	1	AU258458
C	27	11.6	58.0	38	11	AZ776209
C	28	11.6	58.0	39	14	BX289673
C	29	11.6	58.0	42	11	BH909732
C	30	11.6	58.0	44	14	AL771809
C	31	11.6	58.0	46	14	BX535253
C	32	11.6	58.0	47	11	AZ321341
C	33	11.6	58.0	48	11	AZ797513
C	34	11.6	58.0	49	11	AZ450961
C	35	11.4	57.0	44	14	DX060578
C	36	11.4	57.0	44	10	R60473
C	37	11.2	56.0	28	10	CT798230
C	38	11.2	56.0	30	12	CT798230
C	39	11.2	56.0	35	11	AZ806105
C	40	11.2	56.0	37	11	AZ592491
C	41	11.2	56.0	37	12	CG715229
C	42	11.2	56.0	37	14	AG199668
C	43	11.2	56.0	40	11	BH405909
C	44	11.2	56.0	40	11	BH904515
C	45	11.2	56.0	45	1	AA276118

ALIGNMENTS

RESULT 1	AZ352012	26 bp	DNA	linear	GSS 29-SEP-2000
LOCUS	1M0090M13P	Mouse 10kb plasmid	UUGCLM library	Mus musculus genomic	
DEFINITION	clone UUGCLM0090M13 F, genomic survey sequence.				
ACCESSION	AZ352012				
VERSION	AZ352012.1	GI:10431249			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 26)				
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0090 row: M column: 13 Seq primer: CGTTGTAACGACGCCAGT Class: plasmid ends High quality sequence stop: 26. Location/Qualifiers 1..26 /organism="Mus musculus" /mol_type="genomic DNA" /strain="CS7BL/6J" /db_xref="taxon:10090" /clone="UUGCLM0090M13" /sex="Male"				
FEATURES	source				

/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 72.0%; Score 14.4; DB 11; Length 26;
 Best Local Similarity 93.8%; Pred. No. 1.5e+04;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17
 |||||
 Db 2 GAGCTCACATCTCCAA 17

RESULT 2

AZ860255/c
 LOCUS 47 bp DNA linear GSS 21-FEB-2001
 DEFINITION 2M0166004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0166J04 F, genomic survey sequence.

ACCESSION AZ860255
 VERSION AZ860255.1 GI:13055225
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 47)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0166 row: J column: 04

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 47.

Location/Qualifiers

1. .47

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0166J04"

FEATURES

source

1. 49

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1909097"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 71.0%; Score 14.2; DB 11; Length 47;
 Best Local Similarity 84.2%; Pred. No. 2.2e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAACTC 20
 |||||
 Db 47 GAGCAAGCATCTCCAACTC 29

RESULT 3

A1348359/c

LOCUS

DEFINITION

Q020F09.x1 NCI CGAP Lu5 Homo sapiens CDNA clone IMAGE:1909097 3,

similar to SW:NMA_HUMAN Q13145 PUTATIVE TRANSMEMBRANE PROTEIN NMA

PRECURSOR. ; mRNA sequence.

ACCESSION A1348359

VERSION A1348359.1 GI:4085565

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 696 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. 49

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1909097"

```

/tissue_type="carcinoid"
/lab_host="DH108"
/clone_lib="NCI_CGAP_Lu5"
/notes="Organ: lung; Vector: pT73D-PacI; 1st strand cDNA
was prepared from neuroendocrine lung carcinoma, and was
then primed with a Not I - oligo(dT) primer.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library is
normalized. Library was constructed by Bento Soares and M.
Fatima Bonaldo."

```

ORIGIN

```

Query Match      69.0%; Score 13.8; DB 1; Length 49;
Best Local Similarity 88.2%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 GGAGCTAACATCTCCAA 17

Db 38 GTAGCTAACTCTCCAA 22

RESULT 4

```

CA795439/c
LOCUS      50 bp mRNA linear EST 05-DEC-2002
DEFINITION Cac_BL_2476 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac_BL_2476 5', mRNA sequence.
ACCESSION CA795439
VERSION    CA795439.1 GI:26052515
KEYWORDS   EST.
SOURCE     Theobroma cacao (cacao)
ORGANISM   Theobroma cacao

```

1 (bases 1 to 50)

```

Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
Retzel,E.R. and Jones,C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
Planta 216 (2), 255-264 (2002)
12447539
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.

```

FEATURES

```

source
1..50
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac_BL_2476"
/issue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
Cacao)"
/notes="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

```

ORIGIN

```

Query Match      67.0%; Score 13.4; DB 4; Length 50;
Best Local Similarity 93.3%; Pred. No. 5.8e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 2 GAGTAACATCTCCA 16

Db 43 GAGTAACACCTCCA 29

RESULT 5

```

AZ362217
LOCUS      47 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0107B16P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0107B16 F, genomic survey sequence.
ACCESSION AZ362217
VERSION    AZ362217.1 GI:10475917
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Published (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: B column: 16
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 47.

```

FEATURES

```

source
1..47
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0107B16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      66.0%; Score 13.2; DB 11; Length 47;
Best Local Similarity 83.3%; Pred. No. 7.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 3 AGCTAACATCTCCAAGTC 20

|||||

DB 18 AGATAACATTTACAAAGTC 35

RESULT 6
LOCUS CT391862
DEFINITION Sus scrofa genomic clone pigE-4888, genomic survey sequence.
ACCESSION CT391862
VERSION CT391862.1 GI:79619301
KEYWORDS GSS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 47)
AUTHORS Humphray, S.J., Plumb, R.W. and Durham, J.L.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the SP6 end of BAC 4888. 4888 is part of the PigEBAC BAC Library created by Roslin Institute/RFCGR. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.

FEATURES
source Location/Qualifiers
1..47
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="pigE-4888"
/tissue_type="Blood cells"
/note="vector pBelOBAC11 sex male"

ORIGIN
Query Match 66.0%; Score 13.2; DB 14; Length 47;
Best Local Similarity 83.3%; Pred. No. 7.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 AGCTACATCTTCAAGTC 20
|||||
DB 10 AGCTGACATGTCAAAGTC 27
|||||

RESULT 7
LOCUS CC888587/c
DEFINITION SALK_152070.41.70.x Arabidopsis thaliana TDNA insertion lines
ACCESSION CC888587
VERSION CC888587.1 GI:33365375
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 49)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At3g22540.
Class: TDNA tagged.
Location/Qualifiers
1..49
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_152070.41.70.x"
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 66.0%; Score 13.2; DB 12; Length 49;
Best Local Similarity 83.3%; Pred. No. 7.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GAGCTAACATCTCCAAAGT 19
|||||
DB 21 GATCTAACACCAACCAAGT 4
|||||

RESULT 8
LOCUS AZ774523
DEFINITION 2M0004L06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004L06 F, genomic survey sequence.
ACCESSION AZ774523
VERSION AZ774523.1 GI:12900062
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0004 row: L column: 06
Seq primer: CTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0004L06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 64.0%; Score 12.8; DB 11; Length 41;
 Best Local Similarity 87.5%; Pred. No. 1.1e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCA 16
 ||||| ||||| |||||
 Db 24 GGGGCTTACATCTCCA 9

RESULT 11

CC795628/c
 LOCUS
 DEFINITION SALK_087613.35.10.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_087613.35.10.x, genomic survey sequence.

ACCESSION CC795628
 VERSION CC795628.1
 KEYWORDS GI:32390851

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE

1 (bases 1 to 28)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

AUTHORS

A Sequence-Indexed Library of Insertion Mutations in the

TITLE

JOURNAL

COMMENT

Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

FEATURES

source

Location/Qualifiers

1..28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_087613.35.10.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 63.0%; Score 12.6; DB 12; Length 28;
 Best Local Similarity 78.9%; Pred. No. 1.3e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGT 19
 ||||| ||||| |||||
 Db 21 GAATCTAAGATCAACCAAGT 3

RESULT 12

LOCUS

DEFINITION

AI194779/c
 ui56e12.x1 Sugano mouse liver mlia Mus musculus cDNA clone
 IMAGE:1886446.3' similar to SW:FI6P_RAT FI9112

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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COMMENT

```

LOCUS          CZ917814          28 bp      DNA          linear      GSS 08-AUG-2005
DEFINITION     4021007A12.2SLy1 4021 - RescueMu Grid V Zea mays genomic, genomic
survey sequence.
ACCESSION      CZ917814
VERSION        CZ917814.1  GI:71936909
KEYWORDS       GSS.
SOURCE         Zea mays
ORGANISM       Zea mays
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
               clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 28)
TITLE          Walbot, V.
AUTHORS        Zea mays
JOURNAL        Maize genomic sequences found using engineered RescueMu transposon
COMMENT        Unpublished (2001)
               Department of Biological Sciences
               Stanford University
               855 California Ave, Palo Alto, CA 94304, USA
               Tel: 650 723 2227
               Fax: 650 725 8221
               Email: walbot@stanford.edu
               Possible ligation site of ends cut by 2 different endonucleases.
               Reverse complemented post-ligation sequence from source sequence.
               Plate: 4021007 row: A column: 12
               Class: transposon-tagged.
               Location/Qualifiers
                 1..28
                   /organism="Zea mays"
                   /mol_type="genomic DNA"
                   /cultivar="mixed background W23/Al88/B73/K55"
                   /db_xref="taxon:4577"
                   /dev_stage="adult"
                   /tissue_type="leaf"
                   /lab_host="DH10B"
                   /clone_lib="4021 - RescueMu Grid V"
                   /notes="Organ: leaf; Vector: RescueMu (engineered from
                   pBluescript backbone); Site 1: BamHI; Site 2: BglII;
                   RescueMu is a 4.9 kb, modified maize Mu transposon
                   designed to allow plasmid rescue from total genomic DNA.
                   Mu elements insert preferentially into transcription
                   units. For more information on RescueMu, go to the web
                   site 'http://www.mutransposon.org/project/RescueMu/'. Grid
                   V was grown at University of Arizona in 2003. DNA was
                   extracted from leaf strips, double digested using BamHI
                   and BglII, and ligated to form circular plasmids. DH10B
                   cells were transformed and then screened on LB plates with
                   ampicillin."

ORIGIN
Query Match          61.0%; Score 12.2; DB 13; Length 28;
Best Local Similarity 82.4%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  GAGCTAACATCTCCAAG 18
    |||
DB   2  GAAGTCACATCTCCAAG 18

RESULT 14
BZ381186/c          35 bp      DNA          linear      GSS 26-NOV-2002
LOCUS              SALK_116379.23.70.x Arabidopsis thaliana TDNA insertion lines
DEFINITION         Arabidopsis thaliana genomic clone SALK_116379.23.70.x, genomic
survey sequence.
ACCESSION          BZ381186
VERSION            BZ381186.1  GI:25474862
KEYWORDS           GSS.
SOURCE             Arabidopsis thaliana
ORGANISM           Arabidopsis thaliana (thale cress)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

1 (bases 1 to 35)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinac, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
               Location/Qualifiers
                 1..35
                   /organism="Arabidopsis thaliana"
                   /mol_type="genomic DNA"
                   /ecotype="Col-0"
                   /db_xref="taxon:3702"
                   /clone_lib="SALK_116379.23.70.x"
                   /notes="Arabidopsis thaliana TDNA insertion lines"
                   /note="PCR was performed on Arabidopsis thaliana lines
                   notes of which contains one or more TDNA insertion
                   elements. The resultant fragment for each line was
                   directly sequenced to determine the genomic sequence at
                   the site of insertion. Details of the protocols used can
                   be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          61.0%; Score 12.2; DB 11; Length 35;
Best Local Similarity 82.4%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1  GGAGCTAACATCTCCA 17
    |||
DB   1  GGTGCTAATAGCTCCA 1

RESULT 15
AZ989635
LOCUS              2M0273K06F Mouse 10kb plasmid TUGC2M library Mus musculus genomic
clone UUGC2M0273K06 F, genomic survey sequence.
DEFINITION         AZ989635
VERSION            AZ989635.1  GI:13860862
KEYWORDS           GSS.
SOURCE             Mus musculus (house mouse)
ORGANISM           Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE          1 (bases 1 to 37)
AUTHORS            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
               Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
               Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
               Niederhausern, A. and Wright, D., Weises, R.
               Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
               Unpublished (2000)
               Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0273 row: K column: 06

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Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 37.

Location/Qualifiers

source

1..37
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0273K06"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 61.0%; Score 12.2; DB 11; Length 37;
Best Local Similarity 82.4%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCCAAGTC 20
|||||
Db 2 GCTAACATCTCCCGCC 18

Search completed: May 21, 2006, 23:02:41
Job time : 2201 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 22:08:44 ; Search time 115.5 Seconds
(without alignments)
324.002 Million cell updates/sec

Title: US-10-766-185-4
Perfect score: 20
Sequence: 1 ggagctacatctccaagtc 20

Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1429044

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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5: /EMC_Celerra_SID33/ptodata/2/ina/7_COMB.seq:*
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7: /EMC_Celerra_SID33/ptodata/2/ina/PCUTUS_COMB.seq:*
8: /EMC_Celerra_SID33/ptodata/2/ina/PP_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	13.8	69.0	25	3	US-09-396-196G-88908
3	13.6	68.0	30	5	US-09-501-328-19
4	13.6	68.0	40	3	US-09-014-416-19
5	13.6	68.0	41	3	US-09-014-416-50
6	13.6	68.0	42	3	US-09-014-416-51
7	13.4	67.0	20	3	US-09-198-452A-3110
8	13.4	67.0	25	3	US-09-396-196G-87226
9	13	65.0	25	3	US-09-396-196G-88906
10	12.8	64.0	24	3	US-10-002-974-76
11	12.8	64.0	24	3	US-10-002-974-77
12	12.8	64.0	29	3	US-09-214-718-13
13	12.8	64.0	47	3	US-09-423-978-1943
14	12.8	64.0	50	3	US-10-131-827-4910
15	12.8	64.0	50	5	US-10-131-831-4910
16	12.6	63.0	21	3	US-09-657-472-2547
17	12.6	63.0	25	3	US-09-396-196G-25961
18	12.6	63.0	25	3	US-09-396-196G-74047
19	12.6	63.0	26	3	US-09-014-416-18
20	12.6	63.0	30	4	US-10-206-406A-20
21	12.6	63.0	38	3	US-09-474-432B-1384
22	12.6	63.0	38	3	US-09-476-387-1383
23	12.6	63.0	39	2	US-08-537-002A-15

c 24	12.6	63.0	39	3	US-08-863-010-15	Sequence 15, Appl
c 25	12.6	63.0	39	3	US-09-024-429-15	Sequence 15, Appl
c 26	12.6	63.0	39	10	5256648-8	Patent No. 5256648
c 27	12.4	62.0	20	2	US-08-117-952-674	Sequence 674, App
c 28	12.4	62.0	25	3	US-09-396-196G-13583	Sequence 13583, A
c 29	12.4	62.0	25	3	US-09-396-196G-34775	Sequence 34775, A
c 30	12.4	62.0	25	3	US-09-396-196G-34776	Sequence 34776, A
c 31	12.4	62.0	25	3	US-09-396-196G-34919	Sequence 34919, A
c 32	12.4	62.0	25	3	US-09-396-196G-34920	Sequence 34920, A
c 33	12.4	62.0	25	3	US-09-396-196G-34931	Sequence 34931, A
c 34	12.4	62.0	25	3	US-09-396-196G-34932	Sequence 34932, A
c 35	12.4	62.0	25	3	US-09-396-196G-34933	Sequence 34933, A
c 36	12.4	62.0	25	3	US-09-396-196G-34934	Sequence 34934, A
c 37	12.4	62.0	25	3	US-09-396-196G-115104	Sequence 115104, A
c 38	12.4	62.0	27	3	US-09-579-420B-7	Sequence 7, Appl
c 39	12.4	62.0	27	3	US-09-579-420B-9	Sequence 9, Appl
c 40	12.4	62.0	27	3	US-09-579-420B-11	Sequence 11, Appl
c 41	12.4	62.0	27	3	US-09-579-420B-13	Sequence 13, Appl
c 42	12.4	62.0	27	3	US-09-579-420B-14	Sequence 14, Appl
c 43	12.4	62.0	27	3	US-10-101-816-10	Sequence 10, Appl
c 44	12.4	62.0	27	3	US-10-101-816-11	Sequence 11, Appl
c 45	12.4	62.0	30	3	US-09-421-365-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-396-196G-88907
; Sequence 88907, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88907
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88907

Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCTAACATCTCCCAAGTC 20
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Db 7 GCTAACATCTCCATTC 23

RESULT 2
US-09-396-196G-88908
; Sequence 88908, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678


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; PRIOR FILING DATE: 1998-09-17
;
; NUMBER OF SEQ ID NOS: 127806
;
; SOFTWARE: FastSeq for Windows
; SEQ ID NO 88908
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88908

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Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels

QY .
4 GCTAACATCTCCAAGTC 20
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Db
1 GCTAACATCTCCATTTC 17

RESULT 3
US-09-501-328-19

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: Sequence 19, Application US/09501328
: Patent No. 702320
: GENERAL INFORMATION:
: APPLICANT: Macklin, Michael D.
: APPLICANT: Fuller, Deborah L.
: TITLE OF INVENTION: MYCOBACTERIUM
: FILE REFERENCE: 7011-0032
: CURRENT APPLICATION NUMBER: US/09/5
: CURRENT FILING DATE: 2000-02-09
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 19
: LENGTH: 30

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Query Match 68.0%; Score 13.6; DB 5; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels

QY 1 GGAGCTAACATCTCCAAGTC 20
||||| ||| ||||| |
Db 1 GGAGCTAGCATGGCCCAAGAC 20

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RESULT 4
US-09-014-416-19/c
; Sequence 19, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Bukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; TITLE OF INVENTION: US9 THEREOF
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-19

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Query Match 68.0%; Score 13.6; DB 3; Length 40;
Best Local Similarity 80.0%;
Matches 16; Conservative 0; Mismatches 4; Indels
Pred. NO. 1.5e+03;

Qy 1 GGAGCTAACATCTCCAAGTC 20
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Db 33 GGAGCTAACCACTCCAGGCC 14

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RESULT 5
US-09-014-416-50
; Sequence 50, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Bukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-50

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Query Match      68.0%; Score 13.6; DB 3; Length 41;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1 GGAGCTAACATCTCTCCAAGTC 20
8 GGAGCTAACCTCCAGGCC 27

```

RESULT 6
US-09-014-416-51
; Sequence 51, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Eukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-51

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Query Match      68.0%; Score 13.6; DB 3; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 GGAGCTAACATCTCCAAGTC 20
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Db 8 GGAGCTAACCACTCCAGGCC 27

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; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88906
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88906

Query Match      65.0%; Score 13; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GCTAACATCTCCAA 16
DB      13 GCTAACATCTCCAA 25

RESULT 7
US-09-198-452A-3110
; Sequence 3110, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3110
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3110

Query Match      67.0%; Score 13.4; DB 3; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCTAACATCTCCAAG 18
DB      6 GCTGACATCTCCAAG 20

RESULT 8
US-09-396-196G-87226/c
; Sequence 87226, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87226
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-87226

Query Match      67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GAGCTAACATCTCCA 16
DB      22 GAGCTAAGATCTCCA 8

RESULT 9
US-09-396-196G-88906
; Sequence 88906, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
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; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88906
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88906

Query Match      65.0%; Score 13; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GCTAACATCTCCAA 16
DB      13 GCTAACATCTCCAA 25

RESULT 10
US-10-002-974-76/c
; Sequence 76, Application US/10002974
; Patent No. 6858391
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogur, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan L
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UN-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-002-974-76

Query Match      64.0%; Score 12.8; DB 3; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAGCTAACATCTCCAA 17
DB      16 GAGCTAACTCTGCAA 1

RESULT 11
US-10-002-974-77/c
; Sequence 77, Application US/10002974
; Patent No. 6858391
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogur, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan L
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UN-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 24
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-002-974-77

Query Match          64.0%; Score 12.8; DB 3; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17
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Db 16 GAGCTAACATCTGCAA 1

RESULT 12
US-09-214-718-13
; Sequence 13, Application US/09214718
; Patent No. 6756357
; GENERAL INFORMATION:
; APPLICANT: Laufer, Ralph
; APPLICANT: Di Marco, Annalise
; TITLE OF INVENTION: VARIANTS OF HUMAN CILIARY NEUROTROPHIC
; TITLE OF INVENTION: FACTOR (hcnf) WITH A RANGE OF ACTION DIFFERENT FROM THAT OF
; TITLE OF INVENTION: THE WILD-TYPE MOLECULE
; FILE REFERENCE: ITR0009P
; CURRENT APPLICATION NUMBER: US/09/214,718
; CURRENT FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: PCT/IT97/00163
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: RM96A000492
; PRIOR FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-214-718-13

Query Match          64.0%; Score 12.8; DB 3; Length 29;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17
   ||||| ||||| |||||
Db 13 GAGCCACCATCTCCAA 28

RESULT 13
US-09-422-978-1943/c
; Sequence 1943, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1943
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
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; LOCATION: 24
; OTHER INFORMATION: 99-7493-249 : polymorphic base G or C
US-09-422-978-1943

Query Match          64.0%; Score 12.8; DB 3; Length 47;
Best Local Similarity 87.5%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGT 19
   ||||| ||||| |||||
Db 19 GGTCAATCTCCAAGT 4

RESULT 14
US-10-131-827-4910/c
; Sequence 4910, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: LV, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4910
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4910

Query Match          64.0%; Score 12.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17
   ||||| ||||| |||||
Db 32 GAGCTAATATCTCAA 17

RESULT 15
US-10-131-831-4910/c
; Sequence 4910, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: LV, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4910
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-4910
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Query Match 64.0%; Score 12.8; DB 5; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17
|||||
Db 32 GAGCTAATATCTCATA 17

Search completed: May 21, 2006, 23:25:17
Job time : 116.5 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 22:09:18 ; Search time: 654 Seconds
(without alignments)
375.769 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggagtaacatctccaagtc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24111450

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq*
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- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	20	8	US-10-766-185-3
2	20	100.0	20	8	US-10-766-185-4
3	16	80.0	16	8	US-10-407-807-13
C 4	15.8	79.0	25	8	US-10-719-956-576763
C 5	15.8	79.0	25	9	US-10-719-900-163104
C 6	15.4	77.0	25	9	US-10-719-900-213846
7	15.4	77.0	25	11	US-10-932-182A-23140
C 8	15.2	76.0	25	11	US-10-932-182A-107428
C 9	15.2	76.0	25	13	US-11-036-317-197855
C 10	15.2	76.0	25	13	US-11-036-317-229502
C 11	15.2	76.0	25	13	US-11-036-317-292030
C 12	15.2	76.0	25	13	US-11-036-317-321919
C 13	15.2	76.0	25	15	US-11-121-849-110453
C 14	15	75.0	50	16	US-11-175-859-56177
C 15	14.8	74.0	19	14	US-11-083-784-429065
16	14.8	74.0	19	14	US-11-083-784-1271642
17	14.8	74.0	19	15	US-11-101-244-429065

18	14.8	74.0	19	15	US-11-101-244-1271642	Sequence 1271642,
19	14.8	74.0	25	8	US-10-719-956-343202	Sequence 343202,
20	14.8	74.0	25	8	US-10-719-956-372970	Sequence 372970,
21	14.8	74.0	25	8	US-10-719-956-556264	Sequence 556264,
C 22	14.8	74.0	25	9	US-10-719-900-135850	Sequence 135850,
23	14.8	74.0	25	9	US-10-719-900-472809	Sequence 472809,
24	14.8	74.0	25	9	US-10-719-900-789532	Sequence 789532,
25	14.8	74.0	25	15	US-11-121-849-362173	Sequence 362173,
26	14.8	74.0	25	15	US-11-121-849-665524	Sequence 665524,
27	14.8	74.0	25	15	US-11-121-849-665525	Sequence 665525,
28	14.4	72.0	19	14	US-11-083-784-163892	Sequence 163892,
29	14.4	72.0	19	14	US-11-083-784-1271671	Sequence 1271671,
30	14.4	72.0	19	15	US-11-101-244-163892	Sequence 163892,
31	14.4	72.0	19	15	US-11-101-244-1271671	Sequence 1271671,
32	14.4	72.0	25	8	US-10-719-956-39265	Sequence 39265, A
C 33	14.4	72.0	25	9	US-10-719-900-455139	Sequence 455139,
34	14.4	72.0	25	10	US-10-956-157-164931	Sequence 164931,
35	14.4	72.0	25	13	US-11-036-317-684060	Sequence 684060,
36	14.4	72.0	25	13	US-11-036-317-787730	Sequence 787730,
C 37	14.4	72.0	25	15	US-11-121-849-98792	Sequence 98792, A
C 38	14.4	72.0	25	15	US-11-121-849-386481	Sequence 386481,
39	14.4	72.0	50	16	US-11-175-859-13104	Sequence 13104, A
40	14.2	71.0	19	14	US-11-083-784-240931	Sequence 240931,
41	14.2	71.0	19	14	US-11-083-784-256488	Sequence 256488,
42	14.2	71.0	19	14	US-11-083-784-256505	Sequence 256505,
43	14.2	71.0	19	15	US-11-101-244-240931	Sequence 240931,
44	14.2	71.0	19	15	US-11-101-244-256488	Sequence 256488,
45	14.2	71.0	19	15	US-11-101-244-256505	Sequence 256505,

ALIGNMENTS

RESULT 1

US-10-766-185-3/c
; Sequence 3, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
; APPLICANT: Yoon, Heejeong
; APPLICANT: Ahn, Chang Ho
; APPLICANT: Lee, Young Bok
; APPLICANT: Mao, Lingjun
; APPLICANT: Jiang, Xiaoming
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
; FILE REFERENCE: REX 7034
; CURRENT APPLICATION NUMBER: US/10/766,185
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
US-10-766-185-3

Query Match

Best Local Similarity 100.0%; Score 20; DB 8; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGTAAATCTCCAAGTC 20

DB 20 GGAGTAAATCTCCAAGTC 1

RESULT 2

US-10-766-185-4
; Sequence 4, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
; APPLICANT: Yoon, Heejeong
; APPLICANT: Ahn, Chang Ho
; APPLICANT: Lee, Young Bok
; APPLICANT: Mao, Lingjun

/ APPLICANT: Jiang, Xiaoming
/ TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
/ FILE REFERENCE: REX 7034
/ CURRENT APPLICATION NUMBER: US/10/766,185
/ CURRENT FILING DATE: 2004-01-28
/ NUMBER OF SEQ ID NOS: 130
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: antisense oligonucleotide
US-10-766-185-4

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
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Db 1 GGAGCTAACATCTCCAAGTC 20

RESULT 3
US-10-407-807-13
/ Sequence 13, Application US/10407807
/ Publication No. US20040096848A1
/ GENERAL INFORMATION:
/ APPLICANT: THRUB, CHARLOTTE ALBAEK
/ APPLICANT: HOG, ANJA MOLHART
/ APPLICANT: KRISTJANSEN, PAUL E.G.
/ TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION HIF-1ALPHA
/ FILE REFERENCE: 57390 (45120)
/ CURRENT APPLICATION NUMBER: US/10/407,807
/ CURRENT FILING DATE: 2003-10-23
/ PRIOR APPLICATION NUMBER: 60/370,126
/ PRIOR FILING DATE: 2002-04-05
/ NUMBER OF SEQ ID NOS: 124
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 13
/ LENGTH: 16
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: oligonucleotide
US-10-407-807-13

Query Match 80.0%; Score 16; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGT 19
|||||
Db 1 GCTAACATCTCCAAGT 16

RESULT 4
US-10-719-956-576763/c
/ Sequence 576763, Application US/10719956
/ Publication No. US20040146910A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

/ SEQ ID NO 576763
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-10-719-956-576763

Query Match 79.0%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAAGTC 20
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Db 22 GAGCGAACATTTCCAAGTC 4

RESULT 5
US-10-719-900-163104/c
/ Sequence 163104, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 163104
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-163104

Query Match 79.0%; Score 15.8; DB 9; Length 25;
Best Local Similarity 89.5%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGT 19
|||||
Db 24 GGAGCGAACATCTCCAAGT 6

RESULT 6
US-10-719-900-213846/c
/ Sequence 213846, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 213846
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-213846

Query Match 77.0%; Score 15.4; DB 9; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGTC 20
|||||
Db 24 GCTAACATCTCCAAGTC 8

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RESULT 7
US-10-932-182A-23140
; Sequence 23140, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23140
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-23140

Query Match          77.0%; Score 15.4; DB 11; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCCAAGTC 20
DB 5 GCTAGATCTCCCAAGTC 21

RESULT 8
US-10-932-182A-107428
; Sequence 107428, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107428
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-107428

Query Match          76.0%; Score 15.2; DB 11; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
DB 5 GGTGCTAAGATCACCACAGTC 24

RESULT 9
US-11-036-317-197855/c
; Sequence 197855, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 292030
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-197855/c

Query Match          76.0%; Score 15.2; DB 13; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 10
US-11-036-317-229502/c
; Sequence 229502, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 229502
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-229502

Query Match          76.0%; Score 15.2; DB 13; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
DB 22 GGAGATGACATGTCCCAAGTC 3

RESULT 11
US-11-036-317-292030/c
; Sequence 292030, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 292030
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-292030

Query Match          76.0%; Score 15.2; DB 13; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 GGAGCTAACATCTCCCAAGTC 20
    |||||
Db 20 GGAGATGACATGTCCCAAGTC 1

RESULT 12
US-11-036-317-321919/c
; Sequence 321919, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 321919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-321919

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 13; Length 25;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
    |||||
Db 21 GGAGATGACATGTCCCAAGTC 2

RESULT 13
US-11-121-849-110453
; Sequence 110453, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-110453

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 15; Length 25;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
    |||||
Db 1 GGAGTACCATCTGCANATC 20

RESULT 14
US-11-175-859-56177/c
; Sequence 56177, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
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; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56177
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-56177
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Query Match
Best Local Similarity 75.0%; Score 15; DB 16; Length 50;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCCAAGTC 20
    |||||
Db 32 GCTAACRTCTCTAAGTC 16
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RESULT 15
US-11-083-784-429065
; Sequence 429065, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 429065
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-429065
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Query Match
Best Local Similarity 74.0%; Score 14.8; DB 14; Length 19;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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QY 2 GAGCTAACATCTCCCAAGT 19
    |||||
Db 1 GAGCUUACUCCUCCAGU 18
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Search completed: May 21, 2006, 22:32:00
Job time : 655 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 22:18:38 ; Search time 32.5 Seconds
(without alignments)
43.419 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggagctaacatctccaagtc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 387544

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database : Published Applications NA New.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15.4	77.0	25	7	US-11-217-529-23140	Sequence 23140, A
2	15.2	76.0	25	7	US-11-217-529-107428	Sequence 107428, A
3	14	70.0	25	7	US-11-217-529-35122	Sequence 35122, A
4	13.8	69.0	25	7	US-11-217-529-70037	Sequence 70037, A
5	13.8	69.0	25	7	US-11-217-529-85327	Sequence 85327, A
6	13.6	68.0	25	7	US-11-217-529-46511	Sequence 46511, A
7	13.2	66.0	25	7	US-11-217-529-134913	Sequence 134913, A
8	12.8	64.0	25	7	US-11-217-529-8091	Sequence 8091, Ap
9	12.8	64.0	25	7	US-11-217-529-131839	Sequence 131839, Ap
10	12.8	64.0	50	6	US-10-511-937-2714	Sequence 2714, Ap
11	12.6	63.0	25	7	US-11-217-529-46927	Sequence 46927, A
12	12.6	63.0	25	7	US-11-217-529-84789	Sequence 84789, A
13	12.6	63.0	25	7	US-11-217-529-129113	Sequence 129113, A
14	12.6	63.0	25	7	US-11-217-529-141646	Sequence 141646, A
15	12.6	63.0	25	7	US-11-217-529-170895	Sequence 170895, A
16	12.6	63.0	27	1	US-09-756-0978-97	Sequence 97, Appl
17	12.6	63.0	30	1	US-09-756-0978-94	Sequence 94, Appl
18	12.4	62.0	25	7	US-11-217-529-9788	Sequence 9788, Ap
19	12.4	62.0	25	7	US-11-217-529-23135	Sequence 23135, A
20	12.4	62.0	25	7	US-11-217-529-117896	Sequence 117896, A
21	12.4	62.0	34	6	US-10-946-650-26	Sequence 26, Appl
22	12.2	61.0	21	7	US-11-264-784-183	Sequence 183, Appl
23	12.2	61.0	25	7	US-11-217-529-9472	Sequence 9472, Ap
24	12.2	61.0	25	7	US-11-217-529-28702	Sequence 28702, A
25	12.2	61.0	25	7	US-11-217-529-33496	Sequence 33496, A

c	26	12.2	61.0	25	7	US-11-217-529-59585	Sequence 59585, A
	27	12.2	61.0	25	7	US-11-217-529-65432	Sequence 65432, A
	28	12.2	61.0	25	7	US-11-217-529-67969	Sequence 67969, A
c	29	12.2	61.0	25	7	US-11-217-529-94140	Sequence 94140, A
	30	12.2	61.0	25	7	US-11-217-529-179468	Sequence 179468, A
	31	12.2	61.0	50	6	US-10-511-937-42	Sequence 42, Appl
	32	12	60.0	21	7	US-11-078-073-598	Sequence 598, App
	33	12	60.0	23	7	US-11-078-073-321	Sequence 321, App
	34	12	60.0	23	7	US-11-078-073-322	Sequence 322, App
	35	12	60.0	23	7	US-11-078-073-323	Sequence 323, App
	36	12	60.0	23	7	US-11-078-073-324	Sequence 324, App
c	37	12	60.0	23	7	US-11-078-073-599	Sequence 599, App
	38	12	60.0	25	7	US-11-217-529-9790	Sequence 9790, Ap
	39	12	60.0	25	7	US-11-217-529-11244	Sequence 11244, A
c	40	12	60.0	25	7	US-11-217-529-41621	Sequence 41621, A
c	41	12	60.0	25	7	US-11-217-529-42036	Sequence 42036, A
	42	12	60.0	25	7	US-11-217-529-122597	Sequence 122597, A
	43	12	60.0	25	7	US-11-217-529-134018	Sequence 134018, A
	44	12	60.0	30	1	US-09-756-0978-91	Sequence 91, Appl
c	45	11.8	59.0	25	7	US-11-217-529-17865	Sequence 17865, A

ALIGNMENTS

RESULT 1
US-11-217-529-23140
; Sequence 23140, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23140
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-23140
Query Match 77.0%; Score 15.4; DB 7; Length 25;
Best Local Similarity 94.1%; Pred.No.6;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GCTAACATCTCCAAGTC 20
|||||
Db 5 GCTAAGATCTCCAAGTC 21
RESULT 2
US-11-217-529-107428
; Sequence 107428, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

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/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 107428
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-107428

Query Match      76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 7.7;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTTAACATCTCCAAGTC 20
Db 5 GGTGCTAAGATCACCAGTC 24

RESULT 3
US-11-217-529-35122
/ Sequence 35122, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 35122
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-35122

Query Match      70.0%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACATCTCCAAGTC 20
Db 4 AACATCTCCAAGTC 17

RESULT 4
US-11-217-529-70037
/ Sequence 70037, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3

/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 70037
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-70037

Query Match      69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTTAACATCTCCAAG 18
Db 3 GAGCTGACATCTTCAAG 19

RESULT 5
US-11-217-529-85327
/ Sequence 85327, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 85327
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-85327

Query Match      69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGTC 20
Db 6 GCTGACATCTCCAAGCC 22

RESULT 6
US-11-217-529-46511
/ Sequence 46511, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 46511
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-46511
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Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAGCTAAACATCTCCCAAGTC 20
||| ||||| ||| |||||
DB 1 GGAACTAACACCTGCCAAGGC 20

RESULT 7
US-11-217-529-134913/c
; Sequence 134913, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 134913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-134913

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAAACATCTCCCAAGT 19
||| ||||| ||| |||||
DB 23 GAGAAACATGCCCAAGT 6

RESULT 8
US-11-217-529-8091/c
; Sequence 8091, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-8091

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGCTAACATCTCCAAG 18
||| ||||| ||| |||||
DB 19 AGGTAACATCACCACAG 4

RESULT 9
US-11-217-529-191839/c
; Sequence 191839, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191839
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-191839

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGCTAACATCTCCAAG 18
||| ||||| ||| |||||
DB 21 AGCTAACACGCTACAAG 6

RESULT 10
US-10-511-937-2714/c
; Sequence 2714, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2714
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2714

Query Match 64.0%; Score 12.8; DB 6; Length 50;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAA 17
    ||||| |||||
Db 32 GAGCTAATATCTCAA 17

RESULT 11
US-11-217-529-46927
; Sequence 46927, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 46927
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-46927

Query Match 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGT 19
    ||||| ||||| |||||
Db 2 GAAGCTGCGCTTCTCCAAGT 20

RESULT 12
US-11-217-529-84789
; Sequence 84789, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 84789
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-84789

Query Match 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 5 GGATCTAACCTCACTAAGT 23

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAA 17
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Db 32 GAGCTAATATCTCAA 17

RESULT 13
US-11-217-529-129113/c
; Sequence 129113, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129113
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-129113

Query Match 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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US-11-217-529-141646/c
; Sequence 141646, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 141646
; LENGTH: 25
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US-11-217-529-141646

Query Match 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 15
US-11-217-529-170895/c
; Sequence 170895, Application US/11217529

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; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 170895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-170895

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Best Local Similarity 78.9%; Pred.No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Search completed: May 21, 2006, 22:34:13
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

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Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 GGAGCTACATCTCCAGTC 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	20	100.0	54	2	BD187041
C 3	20	100.0	57	2	BD187061
C 4	20	100.0	58	2	BD187058
5	20	100.0	58	2	BD187066
C 6	20	100.0	60	2	CQ536778
C 7	20	100.0	66	2	BD187057
C 8	20	100.0	66	2	BD187065
C 9	20	100.0	168	2	BD187042
C 10	20	100.0	716	14	AY843289S6
C 11	20	100.0	996	5	HSRIFIA10
C 12	20	100.0	1335	2	AX147413
C 13	20	100.0	2359	14	AY455802
C 14	20	100.0	2481	2	AX451938
C 15	20	100.0	2481	2	AX481424
C 16	20	100.0	2481	5	BT009776
C 17	20	100.0	2481	8	AY890352
C 18	20	100.0	2509	5	AF304431

C 19	20	100.0	2517	2	AR629787	AR629787 Sequence
C 20	20	100.0	2522	5	AF208487	AF208487 Homo sapi
C 21	20	100.0	2528	2	AX230580	AX230580 Sequence
C 22	20	100.0	2528	2	AX536309	AX536309 Sequence
C 23	20	100.0	2530	5	AF207601	AF207601 Homo sapi
C 24	20	100.0	2537	5	AF207602	AF207602 Homo sapi
C 25	20	100.0	2551	14	AB018398	AB018398 Bos taurus
C 26	20	100.0	3013	14	AY971808	AY971808 Pantholop
C 27	20	100.0	3229	2	AR531606	AR531606 Sequence
C 28	20	100.0	3296	14	AY621118	AY621118 Bos grun
C 29	20	100.0	3551	5	AB073325	AB073325 Homo sapi
C 30	20	100.0	3669	5	AB169332	AB169332 Macaca fa
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C 32	20	100.0	3678	2	AR642334	AR642334 Sequence
C 33	20	100.0	3678	2	AX504300	AX504300 Sequence
C 34	20	100.0	3678	2	AX770508	AX770508 Sequence
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C 36	20	100.0	3736	2	BD222980	BD222980 Stable hy
C 37	20	100.0	3736	2	AR317244	AR317244 Sequence
C 38	20	100.0	3913	2	CQ719027	CQ719027 Sequence
C 39	20	100.0	3927	2	AX321214	AX321214 Sequence
C 40	20	100.0	3933	2	AX763546	AX763546 Sequence
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C 44	20	100.0	3958	2	CS097358	CS097358 Sequence
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LOCUS	BD187062	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.				
DEFINITION	BD187062					
ACCESSION	BD187062.1	GI:31879262				
VERSION	WO 02099104-A/22.					
KEYWORDS	synthetic construct					
SOURCE	other sequences; artificial sequences.					
ORGANISM	1 (bases 1 to 49)					
REFERENCE	Hiraoka,M., Kondo,S. and Harada,M.					
AUTHORS	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it					
TITLE	Patent: WO 02099104-A 22 12-DEC-2002;					
JOURNAL	POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI HARADA					
COMMENT	OS Artificial Sequence					
	PN WO 02099104-A/22					
	PD 12-DEC-2002					
	PF 04-JUN-2002	WO 2002JP005482				
	PR 05-JUN-2001	JP 01P 169948,05-JUN-2001	JP 01P 169949	PI		
	MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA					
	PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00					
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Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
DEFINITION
BD187041
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Hiraoka,M., Kondo,S. and Harada,H.
TITLE
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it
JOURNAL
Patent: WO 02099104-A 1 12-DEC-2002;
POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
HARADA
COMMENT
OS Artificial Sequence
PN WO 02099104-A/1
PD 12-DEC-2002
PF 04-JUN-2002 WO 2002JP005482
PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA
PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
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LOCUS
DEFINITION
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Hiraoka,M., Kondo,S. and Harada,H.
TITLE
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it
JOURNAL
Patent: WO 02099104-A 21 12-DEC-2002;
POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
HARADA
COMMENT
OS Artificial Sequence
PN WO 02099104-A/21
PD 12-DEC-2002
PF 04-JUN-2002 WO 2002JP005482
PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA

Db      26 GGAGCTAACATCTCCAAGTC 45
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BD187041      54 bp DNA linear PAT 17-JUN-2003
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
DEFINITION
BD187041
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Hiraoka,M., Kondo,S. and Harada,H.
TITLE
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
JOURNAL
Patent: WO 02099104-A 1 12-DEC-2002;
POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
HARADA
COMMENT
OS Artificial Sequence
PN WO 02099104-A/1
PD 12-DEC-2002
PF 04-JUN-2002 WO 2002JP005482
PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA
PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 23 GGAGCTAACATCTCCAAGTC 4
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RESULT 3
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LOCUS
DEFINITION
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Hiraoka,M., Kondo,S. and Harada,H.
TITLE
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it
JOURNAL
Patent: WO 02099104-A 21 12-DEC-2002;
POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
HARADA
COMMENT
OS Artificial Sequence
PN WO 02099104-A/21
PD 12-DEC-2002
PF 04-JUN-2002 WO 2002JP005482
PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA

PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
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RESULT 4
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LOCUS
DEFINITION
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Hiraoka,M., Kondo,S. and Harada,H.
TITLE
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it
JOURNAL
Patent: WO 02099104-A 18 12-DEC-2002;
POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
HARADA
COMMENT
OS Artificial Sequence
PN WO 02099104-A/18
PD 12-DEC-2002
PF 04-JUN-2002 WO 2002JP005482
PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA
PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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LOCUS
DEFINITION
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
ACCESSION
VERSION
BD187066.1 GI:31879266

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KEYWORDS      WO 02099104-A/26.
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1 (bases 1 to 58)
AUTHORS       Hiraoka,M., Kondo,S. and Harada,H.
TITLE        Polypeptide causing protein unstable in cell under aerobic
JOURNAL      POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
              HARADA
COMMENT       OS Artificial Sequence
              PN WO 02099104-A/26
              PD 12-DEC-2002
              PF 04-JUN-2002 WO 2002JP005482
              PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
              MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA
              PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
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DEFINITION Sequence 6413 from Patent WO0210449.
ACCESSION  CQ536778
VERSION     CQ536778.1 GI:41503042
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Hukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS     Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE       Oligonucleotide library for detecting rna transcripts and splice
            variants that populate a transcriptome
JOURNAL     Patent: WO 0210449-A 6413 07-FEB-2002;
            CompuGen Inc. (US)
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LOCUS      BD187057
DEFINITION Polypeptide causing protein unstable in cell under aerobic
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VERSION     BD187057.1 GI:31879257
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 66)
AUTHORS     Hiraoka,M., Kondo,S. and Harada,H.
TITLE       Polypeptide causing protein unstable in cell under aerobic
            condition and DNA encoding it
JOURNAL     Patent: WO 02099104-A 17 12-DEC-2002;
            POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
            HARADA
COMMENT     OS Artificial Sequence
            PN WO 02099104-A/17
            PD 12-DEC-2002
            PF 04-JUN-2002 WO 2002JP005482
            PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
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Best Local Similarity 100.0%; Pred. No.18;
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    |||||
Db 28 GGAGCTAACATCTCCCAAGTC 9

RESULT 8
LOCUS      BD187065/c
DEFINITION Polypeptide causing protein unstable in cell under aerobic
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ACCESSION  BD187065
VERSION     BD187065.1 GI:31879265
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 66)
AUTHORS     Hiraoka,M., Kondo,S. and Harada,H.
TITLE       Polypeptide causing protein unstable in cell under aerobic
            condition and DNA encoding it
JOURNAL     Patent: WO 02099104-A 25 12-DEC-2002;
            POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
            HARADA
COMMENT     OS Artificial Sequence
            PN WO 02099104-A/25
            PD 12-DEC-2002
            PF 04-JUN-2002 WO 2002JP005482
            PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
            MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
    |||||
Db 28 GGAGCTAACATCTCCAAGTC 9

RESULT 9
BD187042/c
LOCUS BD187042 168 bp DNA linear PAT 17-JUN-2003
DEFINITION Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
ACCESSION BD187042
VERSION 1 GI:31879242
KEYWORDS WO 02099104-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 168)
AUTHORS Hirakawa,M., Kondo,S. and Harada,H.
TITLES Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it
JOURNAL Patent: WO 02099104-A 2 12-DEC-2002;
POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAKAWA,SHINAE KONDO, HIROSHI
HARADA
COMMENT OS Artificial Sequence
PN WO 02099104-A/2
PD 12-DEC-2002
PR 04-JUN-2002 WO 2002JP005482
PF 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
MASAHIRO HIRAKAWA,SHINAE KONDO,HIROSHI HARADA
PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
CC Description of Artificial Sequence: synthetic DNA FH Key
FT source 1..168
FT Location/Qualifiers
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      1..168
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Best Local Similarity 100.0%; Pred. No. 21;
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QY 1 GGAGCTAACATCTCCAAGTC 20
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Db 50 GGAGCTAACATCTCCAAGTC 31

RESULT 10
AY843289S6/c
LOCUS AY843289S6 716 bp DNA linear MAM 20-JUL-2005
DEFINITION Phoca hispida hypoxia-inducible factor 1alpha gene, exons 11, 12
and partial cds.
ACCESSION AY843294
VERSION AY843294.1 GI:61652850
KEYWORDS 6 of 7
SEGMENT Phoca hispida (ringed seal)
SOURCE Phoca hispida
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

FEATURES
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Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
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RESULT 11
HSH1F1A10/c
LOCUS HSH1F1A10 996 bp DNA linear PRI 26-OCT-1998
DEFINITION Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) gene,
exons 11 and 12.
ACCESSION AF050124
VERSION AF050124.1 GI:3790530
KEYWORDS 10 of 13
SEGMENT Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarctontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 996)
AUTHORS Iyer,N.V., Leung,S.W. and Semenza,G.L.
TITLES The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
evolutionary conservation
JOURNAL Genomics 52 (2), 159-165 (1998)
PUBMED 9782081
REFERENCE 2 (bases 1 to 996)
AUTHORS Iyer,N.V., Leung,S.W. and Semenza,G.L.
TITLES Direct Submission
JOURNAL Submitted (24-FEB-1998) Departments of Pediatrics and Medicine,
Mammalia; Eutheria; Laurasiatheria; Carnivora; Pinnipedia;
Phocidae; Phoca.
REFERENCE 1 (bases 1 to 716)
AUTHORS Johnson,P., Elsner,R. and Zenteno-Savin,T.
TITLES Hypoxia-Inducible Factor in Ringed Seal (Phoca hispida) tissues
JOURNAL Free Radic. Res. 38 (8), 847-854 (2004)
PUBMED 15493458
REFERENCE 2 (bases 1 to 716)
AUTHORS Johnson,P., Elsner,R. and Zenteno-Savin,T.
TITLES Hypoxia-inducible factor 1 proteomics and diving adaptations in
ringed seal
JOURNAL Free Radic. Biol. Med. 39 (2), 205-212 (2005)
PUBMED 15964512
REFERENCE 3 (bases 1 to 716)
AUTHORS Johnson,P., Elsner,R. and Zenteno-Savin,T.
TITLES Direct Submission
JOURNAL Submitted (01-DEC-2004) Biomedical Sciences, Ohio University,
Irvine Hall, Athens, OH 45701, USA
FEATURES
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  exon
  exon
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Best Local Similarity 100.0%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
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Db 372 GGAGCTAACATCTCCAAGTC 353

RESULT 11
HSH1F1A10/c
LOCUS HSH1F1A10 996 bp DNA linear PRI 26-OCT-1998
DEFINITION Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) gene,
exons 11 and 12.
ACCESSION AF050124
VERSION AF050124.1 GI:3790530
KEYWORDS 10 of 13
SEGMENT Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarctontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 996)
AUTHORS Iyer,N.V., Leung,S.W. and Semenza,G.L.
TITLES The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
evolutionary conservation
JOURNAL Genomics 52 (2), 159-165 (1998)
PUBMED 9782081
REFERENCE 2 (bases 1 to 996)
AUTHORS Iyer,N.V., Leung,S.W. and Semenza,G.L.
TITLES Direct Submission
JOURNAL Submitted (24-FEB-1998) Departments of Pediatrics and Medicine,

```

Institute of Genetic Medicine, Johns Hopkins University School of Medicine, 600 N. Wolfe St, Baltimore, MD 21287-3914, USA

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/db_xref="taxon:9606"
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342..468
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469..902
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/number=12
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
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DB 500 GGAGCTAACATCTCCAAGTC 481

RESULT 12

AX147413/c
LOCUS AX147413 1335 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 1 from Patent WO0136616.
ACCESSION AX147413
VERSION AX147413.1 GI:14346570

SYNTHETIC CONSTRUCT

synthetic construct
other sequences; artificial sequences.

REFERENCE

1
Beuzard, Y., Payen, E., Scherman, D. and Bettan, M.
Acid nucleic construct bearing a system regulating the expression of a gene
Patent: WO 0136616-A 1 25-MAY-2001;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR) ; Aventis Pharma S.A. (FR)

FEATURES

source
Location/Qualifiers
1..1335
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CDS

Query Match 100.0%; Score 20; DB 14; Length 2359;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
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Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 749 GGAGCTAACATCTCCAAGTC 730

RESULT 13

AY455802/c
LOCUS AY455802 2359 bp mRNA linear MAM 23-NOV-2003
DEFINITION Canis familiaris hypoxia-inducible factor 1 alpha subunit mRNA, partial cds.
ACCESSION AY455802
VERSION AY455802.1 GI:38374004
KEYWORDS Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 2359)
Spee, B., Penning, L.C. and Rothuizen, J.
Differential gene expression of regenerative and fibrotic pathways in canine hepatic portosystemic shunt and portal vein hypoplasia
Unpublished
REFERENCE 2 (bases 1 to 2359)
Spee, B., Penning, L.C. and Rothuizen, J.
Direct Submission
TITLE Submitted (31-OCT-2003) Dept. of Clinical Sciences of Companion Animals, University Utrecht, Yalelaan 8, Utrecht, UTR 3508TD, Netherlands

FEATURES

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PKVTTASSTPSYDGTSPASPNRAGKGVISCTEKSHPRS PNVLAVTLTQRTIPREE
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
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LELVEKLPADTEAKNPFSTQDTDLDEMLAPYIPMDDDQLRSFDQSLPSLESSASP
ESASPOSTVTFQCTOIQRTANATTTTATTTDELKTVTKDREMEDPRTKNYGSTIEGL
LDLPDDDAPEEAGLAPRLSFLPAGTRILSTAPPTDVSGLDGLHLDGEDVAMAHADA
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Db 1631 GGAGCTAACATCTCCAAGTC 1612

RESULT 14
AX451938/c
LOCUS AX451938 2481 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 3 from Patent WO0212326.
ACCESSION AX451938
VERSION AX451938.1 GI:21698761
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE 1
AUTHORS Poellinger, L., Pereira, T. and Ruas, J.
TITLE Mechanism of conditional regulation of the hypoxia-inducible
factor-1 by the von hippel-lindau tumor suppressor protein
JOURNAL Patent: WO 0212326-A 3 14-FEB-2002;
Angiogenetics Sweden AB (SE)
FEATURES
Location/Qualifiers
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QNTQSFPLRMKCTLTISRGTWNKISATWKVLCTGHIHVYDNTSNQFQCGYKPPMT
CVLICEPIPHPSNIEIPDLSKIFLSRSLDMKFKSYCDERITELMGYPPELLGRSII
EYHALDSDHPTKTHDMFTKGQVTTGQYMLAKRGVYVWETOATVIYNTKNSQPC
IVCVNVVSGIIOHDLIFSLQTECVLKFPVSSDMKMTQLFTKVESEDTSIFDKLKK
EPDALTLAPAAAGDTTISLDFGSNDTDDQLEEVPLVNDVMLPSPNEKLNINLAM
SPLPTAETPKPLRSSADPALNOEVALKLEPNPESLELSFTMPOIODOTPSPSDGSSTQ
SSPENSPSEYCFYVDSMDVNEFKLEVEKLEPAETEAKNPSTQDTDLDEMLAPYI
PMDDFQRLSPFLSSASPSASPSQSTVTFVQQTQIOEPTANATTTTATTDDEL
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Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1691 GGAGCTAACATCTCCAAGTC 1672

Search completed: May 21, 2006, 22:18:16
Job time : 1333 secs

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1691 GGAGCTAACATCTCCAAGTC 1672

RESULT 15
AX481424/c
LOCUS AX481424 2481 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 38 from Patent WO0205693.
ACCESSION AX481424
VERSION AX481424.1 GI:22316338
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE 1
AUTHORS Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, P.
TITLE Method for inhibiting the expression of a target gene
JOURNAL Patent: WO 02055693-A 38 18-JUL-2002;
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:08:55 ; Search time 259.5 Seconds
(without alignments)
537.360 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 GGAGTAACTATCCCAAGTC 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 104899840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	20	13	ADQ88723
C 2	20	100.0	20	13	ADQ88724
C 3	20	100.0	49	8	ABZ76611
C 4	20	100.0	54	8	ABZ71164
C 5	20	100.0	57	8	ABZ76610
C 6	20	100.0	58	8	ABZ76615
C 7	20	100.0	58	8	ABZ76607
C 8	20	100.0	60	6	ABN33665
C 9	20	100.0	66	8	ABZ71180
C 10	20	100.0	66	8	ABZ76614
C 11	20	100.0	168	8	ABZ71165
C 12	20	100.0	1335	4	AArF85323
C 13	20	100.0	1354	14	ABZ31706
C 14	20	100.0	2481	6	ABV78154
C 15	20	100.0	2481	6	ABZ35730
C 16	20	100.0	2481	6	ABK11552
C 17	20	100.0	2481	6	ABX09973
C 18	20	100.0	2481	6	ABL91695

C 19	20	100.0	2487	5	AAS85055	Aas85055 DNA encod
C 20	20	100.0	2517	8	ACC59243	ACC59243 Human HIF
C 21	20	100.0	2528	4	AAS14154	Aas14154 Human HIF
C 22	20	100.0	2528	6	AAD45951	Aad45951 Human hyp
C 23	20	100.0	2528	10	ADD19045	Add19045 HIF-1alph
C 24	20	100.0	2861	6	ABQ54551	Abq54551 Human ova
C 25	20	100.0	3203	12	AD116279	Ad116279 Human nuc
C 26	20	100.0	3229	9	ADA24506	Ada24506 Human CDN
C 27	20	100.0	3229	10	ADJ56307	Adj56307 Human CDN
C 28	20	100.0	3229	10	ADJ56307	Adj56307 Human CDN
C 29	20	100.0	3229	12	ADJ56307	Adj56307 Human CDN
C 30	20	100.0	3551	12	ADJ56307	Adj56307 Human CDN
C 31	20	100.0	3551	13	ADT78443	Adt78443 Human HIF
C 32	20	100.0	3678	2	AAV63210	Aav63210 Nucleic a
C 33	20	100.0	3678	6	AAJ38995	Aaj38995 Human HIF
C 34	20	100.0	3678	6	ABK84267	Abk84267 Human CDN
C 35	20	100.0	3678	8	ACA89893	Aca89893 Gene diff
C 36	20	100.0	3678	10	ABZ83187	Abz83187 Toxicolog
C 37	20	100.0	3678	14	ABD17984	Aed17984 Fibrotic
C 38	20	100.0	3736	2	AAT45937	Aat45937 Human hyp
C 39	20	100.0	3736	3	AZ299537	Aaz299537 DNA encod
C 40	20	100.0	3736	9	ADA18530	Ada18530 Human DNA
C 41	20	100.0	3736	14	AEC09680	Aec09680 Human HIF
C 42	20	100.0	3812	12	ADO26976	Ado26976 Lung smal
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C 44	20	100.0	3933	2	AAx58980	Aax58980 Human tra
C 45	20	100.0	3933	8	ADA03184	Ada03184 Human Hif

ALIGNMENTS

RESULT 1

ADQ88723/c

ID ADQ88723 standard; DNA; 20 BP.

XX

AC ADQ88723;

XX

DT 21-OCT-2004 (first entry)

XX Human hypoxia inducible factor-1 gene fragment seqid 2.

XX RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;

XX cancer; infection; inflammation; tumour formation; ss.

XX Homo sapiens.

XX US2004152655-A1.

XX 05-AUG-2004.

XX 28-JAN-2004; 2004US-00766185.

XX 31-JAN-2003; 2003US-0444367P.

XX (YOON/) YOON H.

XX (MAOL/) MAO L.

XX (LEEV/) LEE Y B.

XX (AHNC/) AHN C.

XX (JIAN/) JIANG X.

XX Yoon H, Mao L, Lee YB, Ahn C, Jiang X;

XX WPI; 2004-561492/54.

XX New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a

XX nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),

XX useful for inhibiting expression of HIF-1 and inducing cytotoxicity in

XX several cancer cells.

XX Example 4; SEQ ID NO 3; 35pp; English.

XX The invention describes a compound, RX-0047 or RX-0149 targeted to a

XX

CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
 CC where the oligonucleotide compound inhibits the expression of human HIF-
 CC 1. Also described are: a method of inhibiting the expression of human HIF-1 in
 CC human cells or tissues; and a method of inducing cytotoxicity in a cancer
 CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a
 CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5,
 CC aatgaccacagtgctcaa 3' and SEQ ID NO. 4, 5' ggagctaacatctccaaagtc 3',
 CC respectively). The compounds are useful for inhibiting the expression of
 CC HIF-1 and inducing the cytotoxicity in several cancer cells. The
 CC antisense compounds are also useful for preventing or delaying infection,
 CC inflammation, or tumour formation. This sequence represents a site on the
 CC HIF-1 to which antisense oligonucleotides can be targeted in order to
 CC control HIF-1 gene expression.

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 SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
 DB 20 GGAGCTAACATCTCCAAAGTC 1
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RESULT 2
 ADQ88724
 ID ADQ88724 standard; DNA; 20 BP.
 AC ADQ88724;
 DT 21-OCT-2004 (first entry)
 XX
 DE Human HIF-1 antisense oligonucleotide RX-0149.
 XX
 KW RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;
 KW cancer; infection; inflammation; tumour formation; ss;
 KW antisense oligonucleotide; antisense technology.
 XX
 OS Homo sapiens.
 XX
 PN US2004152655-A1.
 XX
 PD 05-AUG-2004.
 XX
 PF 28-JAN-2004; 2004US-00766185.
 XX
 PR 31-JAN-2003; 2003US-0444367P.
 XX
 PA (YOON/) YOON H.
 PA (MAOL/) MAO L.
 PA (LEEY/) LEE Y B.
 PA (AHNC/) AHN C.
 PA (JIAN/) JIANG X.
 XX
 PI Yoon H, Mao L, Lee YB, AHN C, JIANG X;
 XX
 DR WPI; 2004-561492/54.
 XX
 PT New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a
 PT nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
 PT useful for inhibiting expression of HIF-1 and inducing cytotoxicity in
 PT several cancer cells.
 XX
 PS Claim 6; SEQ ID NO 4; 35pp; English.
 XX
 CC The invention describes a compound, RX-0047 or RX-0149 targeted to a
 CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
 CC where the oligonucleotide compound inhibits the expression of human HIF-
 CC 1. Also described are: a method of inhibiting the expression of human HIF-
 CC human cells or tissues; and a method of inducing cytotoxicity in a cancer
 CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a
 CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5,

CC aatgaccacagtgctcaa 3' and SEQ ID NO. 4, 5' ggagctaacatctccaaagtc 3',
 CC respectively). The compounds are useful for inhibiting the expression of
 CC HIF-1 and inducing the cytotoxicity in several cancer cells. The
 CC antisense compounds are also useful for preventing or delaying infection,
 CC inflammation, or tumour formation. This sequence represents a human HIF-1
 CC antisense oligonucleotide.

XX
 SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
 DB 1 GGAGCTAACATCTCCAAAGTC 20
 |||||
 |||||

RESULT 3
 ABZ76611
 ID ABZ76611 standard; DNA; 49 BP.
 XX
 AC ABZ76611;
 XX
 DT 30-APR-2003 (first entry)
 XX
 DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:24.
 XX
 KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
 KW NLS; ODD; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200299104-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 04-JUN-2002; 2002WO-JP005482.
 XX
 PR 05-JUN-2001; 2001JP-00169948.
 PR 05-JUN-2001; 2001JP-00169949.
 XX
 PA (POKK) POLA CHEM IND INC.
 PA (HIRA/) HIRAOKA M.
 PA (KOND/) KONDOH S.
 XX
 PI Hiraoka M, Kondoh S, Harada H;
 XX
 DR WPI; 2003-148670/14.
 XX
 PT New DNA encoding a polypeptide imparting relative stability under hypoxic
 PT conditions to proteins within the cell, useful for treatment of cancer
 PT and improvement of microbial fermentation.
 XX
 PS Example; Page 24; 144pp; Japanese.
 XX
 CC The present invention describes DNA encoding a hypoxia-inducible factor 1
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAFYPMDDDFQL
 CC see ABP57669) (I), or encoding a fusion protein containing at least 16
 CC residues of (I), a nuclear localisation signal (NLS), and another
 CC protein, and imparting relative stability under specific conditions of
 CC oxygen concentration within the cell. Also described: (1) vectors
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing
 CC the fusion protein by culture of the transformed cells; (4) detecting
 CC hypoxic conditions in cells by monitoring the stability of the protein
 CC fused to (I) in cells transformed by vectors containing the DNA; (5)
 CC regulating the stability of proteins within the cell by transformation
 CC with the DNA; (6) inhibiting the development of cells under hypoxic
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
 CC tension. (I) has cytosolic activity, and can be used for the

CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
 CC solid tumour, and in gene therapy. (1) can be used in industrial
 CC microbial fermentation, and in medicine, especially in the treatment of
 CC tumours containing hypoxic regions. The present sequence represents a PCR
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)
 CC domain, which is used in an example from the present invention
 XX

SQ Sequence 49 BP; 15 A; 11 C; 10 G; 13 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 8; Length 49;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGCTAACATCTCCAAGTC 20
 |||||
 DB 26 GGAGCTAACATCTCCAAGTC 45

RESULT 4
 ABZ71164/c
 ID ABZ71164 standard; DNA; 54 BP.
 XX AC ABZ71164;

DT 30-APR-2003 (first entry)

DE Hypoxia-inducible factor 1 alpha 557-574 peptide encoding DNA SEQ.2.

KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
 KW tumour; gene; de.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..54

FT /tag= a

FT /partial

FT /product= "HIF-1 alpha 557-574 peptide"

FT /note= "no start or stop codons given"

XX WO200299104-A1.

PN 12-DEC-2002.

PD 04-JUN-2002; 2002WO-JP005482.

PF 05-JUN-2001; 2001JP-00169948.

PR 05-JUN-2001; 2001JP-00169949.

XX (POKK) POLA CHEM IND INC.

PA (HIRA/) HIRAOKA M.

PA (KOND/) KONDOH S.

XX Hiraoka M, Kondoh S, Harada H;

PI WPI; 2003-148670/14.

XX P-PSDB; ABP57669.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic
 PT conditions to proteins within the cell, useful for treatment of cancer
 PT and improvement of microbial fermentation.

PS Claim 3; Page 58; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
 CC see ABP57669) (1), or encoding a fusion protein containing at least 16
 CC residues of (1), a nuclear localisation signal (NLS), and another
 CC protein, and imparting relative stability under specific conditions of
 CC oxygen concentration within the cell. Also described: (1) vectors
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing
 CC the fusion protein by culture of the transformed cells; (4) detecting

CC hypoxic conditions in cells by monitoring the stability of the protein
 CC fused to (1) in cells transformed by vectors containing the DNA; (5)
 CC regulating the stability of proteins within the cell by transformation
 CC with the DNA; (6) inhibiting the development of cells under hypoxic
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
 CC tension. (1) has cytostatic activity, and can be used for the
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
 CC solid tumour, and in gene therapy. (1) can be used in industrial
 CC microbial fermentation, and in medicine, especially in the treatment of
 CC tumours containing hypoxic regions. The present sequence encodes (1) from
 CC the present invention
 XX

SQ Sequence 54 BP; 14 A; 11 C; 11 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGCTAACATCTCCAAGTC 20

|||||

DB 23 GGAGCTAACATCTCCAAGTC 4

RESULT 5

ABZ76610/c

ID ABZ76610 standard; DNA; 57 BP.

XX AC ABZ76610;

DT 30-APR-2003 (first entry)

DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:23.

KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
 KW NLS; ODD; PCR primer; ss.

OS Homo sapiens.

XX WO200299104-A1.

PN 12-DEC-2002.

PD 04-JUN-2002; 2002WO-JP005482.

PF 05-JUN-2001; 2001JP-00169948.

PR 05-JUN-2001; 2001JP-00169949.

XX (POKK) POLA CHEM IND INC.

PA (HIRA/) HIRAOKA M.

PA (KOND/) KONDOH S.

XX Hiraoka M, Kondoh S, Harada H;

PI WPI; 2003-148670/14.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic
 PT conditions to proteins within the cell, useful for treatment of cancer
 PT and improvement of microbial fermentation.

PS Example; Page 24; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
 CC see ABP57669) (1), or encoding a fusion protein containing at least 16
 CC residues of (1), a nuclear localisation signal (NLS), and another
 CC protein, and imparting relative stability under specific conditions of
 CC oxygen concentration within the cell. Also described: (1) vectors
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing
 CC the fusion protein by culture of the transformed cells; (4) detecting
 CC hypoxic conditions in cells by monitoring the stability of the protein

CC fused to (1) in cells transformed by vectors containing the DNA; (5)
 CC regulating the stability of proteins within the cell by transformation
 CC with the DNA; (6) inhibiting the development of cells under hypoxic
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
 CC tension. (1) has cytostatic activity, and can be used for the
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
 CC solid tumour, and in gene therapy. (1) can be used in industrial
 CC microbial fermentation, and in medicine, especially in the treatment of
 CC tumours containing hypoxic regions. The present sequence represents a PCR
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)
 CC domain, which is used in an example from the present invention
 XX
 SQ Sequence 57 BP; 15 A; 12 C; 13 G; 17 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 57;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGCTAACATCTCCAAGTC 20
 |||||
 Db 28 GGAGCTAACATCTCCAAGTC 9

RESULT 6
 ABZ76615
 ID ABZ76615 standard; DNA; 58 BP.

AC ABZ76615;

DT 30-APR-2003 (first entry)

DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:28.

KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
 KW NLS; ODD; PCR primer; ss.

OS Homo sapiens.

PN WO200299104-A1.

PD 12-DEC-2002.

PF 04-JUN-2002; 2002WO-JP005482.

PR 05-JUN-2001; 2001JP-00169948.

PR 05-JUN-2001; 2001JP-00169949.

PA (POKK) POLA CHEM IND INC.

PA (HIRA/) HIRAOKA M.

PA (KOND/) KONDOH S.

PI Hiraoka M, Kondoh S, Harada H;

DR WPI; 2003-148670/14.

PT New DNA encoding a polypeptide imparting relative stability under hypoxic
 PT conditions to proteins within the cell, useful for treatment of cancer
 PT and improvement of microbial fermentation.

PS Example; Page 24; 144pp; Japanese.

CC The present invention describes DNA encoding a hypoxia-inducible factor 1
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLARYIPMDDDFQL
 CC see ABP57669) (1), or encoding a fusion protein containing at least 16
 CC residues of (1), a nuclear localisation signal (NLS), and another
 CC protein, and imparting relative stability under specific conditions of
 CC oxygen concentration within the cell. Also described: (1) vectors
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing
 CC the fusion protein by culture of the transformed cells; (4) detecting
 CC hypoxic conditions in cells by monitoring the stability of the protein

CC fused to (1) in cells transformed by vectors containing the DNA; (5)
 CC regulating the stability of proteins within the cell by transformation
 CC with the DNA; (6) inhibiting the development of cells under hypoxic
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
 CC tension. (1) has cytostatic activity, and can be used for the
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
 CC solid tumour, and in gene therapy. (1) can be used in industrial
 CC microbial fermentation, and in medicine, especially in the treatment of
 CC tumours containing hypoxic regions. The present sequence represents a PCR
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)
 CC domain, which is used in an example from the present invention
 XX
 SQ Sequence 58 BP; 18 A; 13 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 58;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGCTAACATCTCCAAGTC 20
 |||||
 Db 35 GGAGCTAACATCTCCAAGTC 54

RESULT 7
 ABZ76607

ID ABZ76607 standard; DNA; 58 BP.

AC ABZ76607;

DT 30-APR-2003 (first entry)

DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:20.

KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
 KW NLS; ODD; PCR primer; ss.

OS Homo sapiens.

PN WO200299104-A1.

PD 12-DEC-2002.

PF 04-JUN-2002; 2002WO-JP005482.

PR 05-JUN-2001; 2001JP-00169948.

PR 05-JUN-2001; 2001JP-00169949.

PA (POKK) POLA CHEM IND INC.

PA (HIRA/) HIRAOKA M.

PA (KOND/) KONDOH S.

PI Hiraoka M, Kondoh S, Harada H;

DR WPI; 2003-148670/14.

PT New DNA encoding a polypeptide imparting relative stability under hypoxic
 PT conditions to proteins within the cell, useful for treatment of cancer
 PT and improvement of microbial fermentation.

PS Example; Page 23; 144pp; Japanese.

CC The present invention describes DNA encoding a hypoxia-inducible factor 1
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLARYIPMDDDFQL
 CC see ABP57669) (1), or encoding a fusion protein containing at least 16
 CC residues of (1), a nuclear localisation signal (NLS), and another
 CC protein, and imparting relative stability under specific conditions of
 CC oxygen concentration within the cell. Also described: (1) vectors
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing
 CC the fusion protein by culture of the transformed cells; (4) detecting
 CC hypoxic conditions in cells by monitoring the stability of the protein

CC fused to (I) in cells transformed by vectors containing the DNA; (5)
 CC regulating the stability of proteins within the cell by transformation
 CC with the DNA; (6) inhibiting the development of cells under hypoxic
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
 CC tension. (I) has cytostatic activity, and can be used for the
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
 CC solid tumour, and in gene therapy. (I) can be used in industrial
 CC microbial fermentation, and in medicine, especially in the treatment of
 CC tumours containing hypoxic regions. The present sequence represents a PCR
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)
 CC domain, which is used in an example from the present invention
 XX
 SQ Sequence 58 BP; 19 A; 12 C; 12 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 58;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGAGCTAACATCTCCAAGTC 20
 |||||
 Db 35 GGAGCTAACATCTCCAAGTC 54

RESULT 8
 ABN33665/c
 ID ABN33665 standard; DNA; 60 BP.
 AC ABN33665;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:6413.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-IB001903.
 XX
 PR 28-JUL-2000; 2000US-0221607P.
 XX
 PR 02-MAY-2001; 2001US-0287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI; 2002-257383/30.
 XX
 XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.
 XX
 PS Example 1; SEQ ID NO 6413; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridising selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini

CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at fcp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 60 BP; 16 A; 16 C; 10 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 60;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGAGCTAACATCTCCAAGTC 20
 |||||
 Db 51 GGAGCTAACATCTCCAAGTC 32

RESULT 9
 ABZ71180/c
 ID ABZ71180 standard; DNA; 66 BP.
 AC ABZ71180;
 XX
 DT 30-APR-2003 (first entry)
 XX
 DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:19.
 XX
 KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
 KW NLS; ODD; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200299104-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 04-JUN-2002; 2002WO-JP005482.
 XX
 PR 05-JUN-2001; 2001JP-00169948.
 XX
 PR 05-JUN-2001; 2001JP-00169949.
 XX
 PA (POKK) POLA CHEM IND INC.
 PA (HIRA/) HIRAKA M.
 PA (KOND/) KONDOH S.
 XX
 PI Hiraoka M, Kondoh S, Harada H;
 XX
 DR WPI; 2003-148670/14.
 XX
 XX New DNA encoding a polypeptide imparting relative stability under hypoxic
 PT conditions to proteins within the cell, useful for treatment of cancer
 PT and improvement of microbial fermentation.
 XX
 PS Example; Page 23; 144pp; Japanese.
 XX
 CC The present invention describes DNA encoding a hypoxia-inducible factor 1
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYPMDDDFQL
 CC see ABP57669) (I), or encoding a fusion protein containing at least 16
 CC residues of (I), a nuclear localisation signal (NLS), and another
 CC protein, and imparting relative stability under specific conditions of
 CC oxygen concentration within the cell. Also described: (1) vectors
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing
 CC the fusion protein by culture of the transformed cells; (4) detecting
 CC hypoxic conditions in cells by monitoring the stability of the protein
 CC fused to (I) in cells transformed by vectors containing the DNA; (5)

CC regulating the stability of proteins within the cell by transformation
 CC with the DNA; (6) inhibiting the development of cells under hypoxic
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
 CC tension. (1) has cytostatic activity, and can be used for the
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
 CC solid tumour, and in gene therapy. (1) can be used in industrial
 CC microbial fermentation, and in medicine, especially in the treatment of
 CC tumours containing hypoxic regions. The present sequence represents a PCR
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)
 CC domain, which is used in an example from the present invention
 XX
 SQ Sequence 66 BP; 17 A; 14 C; 14 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 66;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
 |||||
 DB 28 GGAGCTAACATCTCCAAGTC 9

RESULT 10
 ABZ76614/c
 ID ABZ76614 standard; DNA; 66 BP.
 XX
 AC ABZ76614;
 XX
 DT 30-APR-2003 (first entry)
 XX
 DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:27.
 XX
 KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
 KW NLS; ODD; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200299104-A1.
 XX
 PD 12-DEC-2002.

PF 04-JUN-2002; 2002WO-JP005482.
 XX
 PR 05-JUN-2001; 2001JP-00169948.
 PR 05-JUN-2001; 2001JP-00169949.
 XX
 PA (POKK) POLA CHEM IND INC.
 PA (HIRA/) HIRAOKA M.
 PA (KOND/) KONDOH S.
 XX
 PI Hiraoka M, Kondoh S, Harada H;
 XX
 DR WPI; 2003-148670/14.

PT New DNA encoding a polypeptide imparting relative stability under hypoxic
 PT conditions to proteins within the cell, useful for treatment of cancer
 PT and improvement of microbial fermentation.

PS Example; Page 24; 144pp; Japanese.
 XX
 CC The present invention describes DNA encoding a hypoxia-inducible factor 1
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPVPMDDDFQL
 CC see ABP57669) (1), or encoding a fusion protein containing at least 16
 CC residues of (1), a nuclear localisation signal (NLS), and another
 CC protein, and imparting relative stability under specific conditions of
 CC oxygen concentration within the cell. Also described: (1) vectors
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing
 CC the fusion protein by culture of the transformed cells; (4) detecting
 CC hypoxic conditions in cells by monitoring the stability of the protein
 CC fused to (1) in cells transformed by vectors containing the DNA; (5)

CC regulating the stability of proteins within the cell by transformation
 CC with the DNA; (6) inhibiting the development of cells under hypoxic
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
 CC tension. (1) has cytostatic activity, and can be used for the
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
 CC solid tumour, and in gene therapy. (1) can be used in industrial
 CC microbial fermentation, and in medicine, especially in the treatment of
 CC tumours containing hypoxic regions. The present sequence represents a PCR
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)
 CC domain, which is used in an example from the present invention
 XX
 SQ Sequence 66 BP; 16 A; 15 C; 15 G; 20 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 66;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
 |||||
 DB 28 GGAGCTAACATCTCCAAGTC 9

RESULT 11
 ABZ71165/c
 ID ABZ71165 standard; DNA; 168 BP.
 XX
 AC ABZ71165;
 XX
 DT 30-APR-2003 (first entry)
 XX
 DE Nucleotide sequence SEQ ID NO:3.
 XX
 KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
 KW tumour; gene; ds.
 XX
 OS Synthetic.
 XX
 PN WO200299104-A1.
 XX
 PD 12-DEC-2002.

PF 04-JUN-2002; 2002WO-JP005482.
 XX
 PR 05-JUN-2001; 2001JP-00169948.
 PR 05-JUN-2001; 2001JP-00169949.
 XX
 PA (POKK) POLA CHEM IND INC.
 PA (HIRA/) HIRAOKA M.
 PA (KOND/) KONDOH S.
 XX
 PI Hiraoka M, Kondoh S, Harada H;
 XX
 DR WPI; 2003-148670/14.

PT New DNA encoding a polypeptide imparting relative stability under hypoxic
 PT conditions to proteins within the cell, useful for treatment of cancer
 PT and improvement of microbial fermentation.

PS Disclosure; Page 59; 144pp; Japanese.
 XX
 CC The present invention describes DNA encoding a hypoxia-inducible factor 1
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPVPMDDDFQL
 CC see ABP57669) (1), or encoding a fusion protein containing at least 16
 CC residues of (1), a nuclear localisation signal (NLS), and another
 CC protein, and imparting relative stability under specific conditions of
 CC oxygen concentration within the cell. Also described: (1) vectors
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing
 CC the fusion protein by culture of the transformed cells; (4) detecting
 CC hypoxic conditions in cells by monitoring the stability of the protein
 CC fused to (1) in cells transformed by vectors containing the DNA; (5)
 CC regulating the stability of proteins within the cell by transformation

CC with the DNA; (6) inhibiting the development of cells under hypoxic
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
 CC tension. (I) has cytostatic activity, and can be used for the
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
 CC solid tumour, and in gene therapy. (I) can be used in industrial
 CC microbial fermentation, and in medicine, especially in the treatment of
 CC tumours containing hypoxic regions. The present sequence represents a
 CC nucleotide sequence given in the exemplification of the present
 CC invention. N.B. The present sequence is given in the sequence listing of
 CC the present invention but is not mentioned further within the
 CC specification

CC Sequence 168 BP; 48 A; 44 C; 31 G; 45 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 168;

Best Local Similarity 100.0%; Pred. No. 3.5; Length 168;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
 DB 50 GGAGCTAACATCTCCCAAGTC 31

RESULT 12

AAF85323/C
 ID AAF85323 standard; DNA; 1335 BP.

AC AAF85323;

XX 23-JUL-2001 (first entry)

DE Nucleotide sequence of tTAK-hH104.

XX Nucleic acid construct; oxygen partial pressure; cellular hypoxia;
 KW anemia; cancer; ischemia; erythropoietin; immunotherapy;
 KW autoimmune disease; hH104; tTAK; ss.

OS Synthetic.

FH Key Location/Qualifiers
 CDS 1..1335
 FT /*tag= a

XX WO200136616-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-FR003207.

XX 18-NOV-1999; 99FR-00014513.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (AVET) AVENTIS PHARMA SA.

PI Beuzard Y, Payen E, Scherman D, Bettan M;

XX WPI; 2001-343818/36.

DR P-PSDB; AAB68415.

PT New nucleic acid construct for controlling expression of target gene,
 PT useful e.g. for treating cancer, is modulated by exogenous
 PT pharmaceutical and oxygen partial pressure.

XX Disclosure; Page 55-57; 60pp; French.

XX The specification describes a nucleic acid construct bearing a system for
 CC regulating the expression of a gene. The nucleic acid construct comprises
 CC at least one sequence encoding a protein that regulates expression of at
 CC least one gene of interest. The activity of this protein is modulated by
 CC presence/absence of a pharmacological agent and the amount of protein
 CC produced depends on the oxygen partial pressure. The constructs are used
 CC to treat conditions associated with cellular hypoxia, especially anemia,

CC cancer and ischemia, specifically where the gene of interest encodes
 CC erythropoietin (but many other suitable genes are listed, e.g. those
 CC encoding single-chain antibodies for immunotherapy of infections or
 CC autoimmune diseases, prodrug-converting enzymes, apoptosis inducers
 CC etc.). The present sequence represents the open reading frame of tTAK-
 CC hH104. The sequence contains a human hH104 fragment, inserted into the
 CC BsiWI site of tTAK. This sequence is used to produce constructs of the
 CC invention

XX Sequence 1335 BP; 377 A; 323 C; 323 G; 312 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 1335;

Best Local Similarity 100.0%; Pred. No. 4.5; Length 1335;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20

DB 749 GGAGCTAACATCTCCCAAGTC 730

RESULT 13

AEC31706/C

ID AEC31706 standard; DNA; 1354 BP.

XX AEC31706;

XX 20-OCT-2005 (first entry)

DE Anoxia controlled transcription factor associated DNA, SEQ ID No.1.

XX transcription factor; transcription; anoxia; gene expression; tumor;
 KW ischemia; heart disease; arthritis; cardiovascular-gen.; cytostatic;
 KW vasotropic; cardiant; antiarthritic; ds.

XX Unidentified.

XX CN1580262-A.

XX 16-FEB-2005.

XX 12-AUG-2003; 2003CN-00142216.

XX 12-AUG-2003; 2003CN-00142216.

XX (UYSH-) UNIV SHANGHAI NO 3 MEDICAL.

XX Ying LQ, Lu J;

XX WPI, 2005-372977/39.

XX Carrier system containing an artificial transcription factor regulated by
 PT oxygen deficit, and its configuration and use.

XX Claim 2; SEQ ID NO 1; 27pp; Chinese.

XX The invention relates to a transcription factor controlled by anoxia. The
 CC transcription factor is produced by a construction method in which GAL4
 CC DNA combines and HIF1 is active. Also described is a carrier system
 CC containing the transcription factor of the invention. The system is
 CC composed of two carriers: (a) one carrier is controlled by anoxia and can
 CC activate targeted gene expression controlled by the GSTATA promoter, (b)
 CC the other carrier contains the GSTATA promoter. The invention allows the
 CC displacement of different promoters and the ability of controlling gene
 CC expression in cells and organisms undergoing anoxia. Different targeted
 CC genes can be coupled into the carrier for the preparation of therapeutic
 CC drugs for tumor, ischemia angiodiopathy and arthritis. This sequence
 CC represents DNA relating to the present invention.

XX Sequence 1354 BP; 448 A; 267 C; 302 G; 337 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 1354;

Best Local Similarity 100.0%; Pred. No. 4.5; Length 1354;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGAGCTAACATCTCCAAAGTC 20
DB 773 GGAGCTAACATCTCCAAAGTC 754

RESULT 14
ABV78154/c
ID ABV78154 standard; DNA; 2481 BP.
XX
AC ABV78154;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human HIF-alpha DNA SEQ ID NO 38.
XX
KW RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;
KW virucide; protozoicide; gene; ds.
XX
OS Homo sapiens.
XX
PN W0200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
XX
PR 26-OCT-2001; 2001DE-01055280.
XX
PR 29-NOV-2001; 2001DE-01058411.
XX
PR 07-DEC-2001; 2001DE-01060151.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
WPI; 2002-590671/63.
XX
PT Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
PS Claim 10; Page 134-135; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA is complementary to (I) and at least one end of dsRNA
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX
SQ Sequence 2481 BP; 829 A; 512 C; 500 G; 640 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 2481;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
DB 1691 GGAGCTAACATCTCCAAAGTC 1672

RESULT 15
ABZ35730/c
ID ABZ35730 standard; DNA; 2481 BP.
XX
AC ABZ35730;

07-FEB-2003 (first entry)
Human HIF-alpha polynucleotide SEQ ID NO 38.
Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
protozoicide; gene expression; antisense; tumour; infection; Plasmodium;
virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
Hepatitis C virus; human papilloma virus; gene; ds.
Homo sapiens.
DE10100588-A1.
18-JUL-2002.
09-JAN-2001; 2001DE-01000588.
09-JAN-2001; 2001DE-01000588.
(RIBO-) RIBOPHARMA AG.
Kreutzer R, Limmer S, Rost S, Hadwiger P;
WPI; 2002-683450/74.
Inhibiting expression of target genes, useful e.g. for treating tumors,
by introducing into cells two double-stranded RNAs that are complementary
to the target.
Claim 13; Page 31; 100pp; German.
The invention relates to inhibiting expression of a target gene in a cell
by introducing at least two oligonucleotides (dsRNA I and II), both
with a double-stranded (ds) structure of at most 49 sequential nucleotide
pairs. At least part of one strand (S1, S2) of the ds structures in each
of dsRNA I and II are complementary to regions in the target gene. The
method uses antisense inhibition of gene expression using double stranded
RNA inhibition (RNAi). The method is particularly used to treat tumours
or infections, especially by Plasmodium or viruses/viroids (pathogenic on
humans, animals or plants). The method provides more effective inhibition
of expression than known methods using a single dsRNA, even at very low
concentrations. When dsRNA has at least one unpaired nucleotide at the
end, stability (and thus effective concentration in the cell) is improved
and efficiency can be increased further by pretreating the cells with
interferon. The present sequence is that of a target DNA of the invention
Sequence 2481 BP; 829 A; 512 C; 500 G; 640 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 2481;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
DB 1691 GGAGCTAACATCTCCAAAGTC 1672

Search completed: May 21, 2006, 21:17:45
Job time : 262.5 secs
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QM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:16:50 ; Search time 2223.5 Seconds
(without alignments)
502.985 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggagctaacatctcccaagtc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_estc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gse1:*
- 12: gb_gse2:*
- 13: gb_gse3:*
- 14: gb_gse4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	110	2	BF900491
2	20	100.0	165	2	BF734487
3	20	100.0	222	10	T10413
4	20	100.0	316	10	DX178075
5	20	100.0	324	8	CN264306
6	20	100.0	326	7	BE184816
7	20	100.0	357	7	AW860808
8	20	100.0	370	7	AW862545
9	20	100.0	387	10	DX137624
10	20	100.0	400	9	D56430
11	20	100.0	421	7	AW800395
12	20	100.0	421	7	BE896421
13	20	100.0	424	10	DX048267
14	20	100.0	445	7	BE896412
15	20	100.0	453	11	AQ805950
16	20	100.0	454	7	BE896416
17	20	100.0	464	3	BM835867
18	20	100.0	467	9	DA163304
19	20	100.0	470	11	AQ813482

20	100.0	472	7	BE896419
21	100.0	486	1	AA937180
22	100.0	493	3	BM754664
23	100.0	495	9	DA659458
24	100.0	503	9	DA551645
25	100.0	514	1	AI921994
26	100.0	522	4	CB267820
27	100.0	528	9	DA653429
28	100.0	529	9	DA871625
29	100.0	534	9	DB013054
30	100.0	542	9	DA490064
31	100.0	549	9	DA944956
32	100.0	550	9	DA363361
33	100.0	550	9	DA882416
34	100.0	551	9	DA952887
35	100.0	553	9	DA665410
36	100.0	553	9	DA693441
37	100.0	556	9	DA487729
38	100.0	558	9	DA596431
39	100.0	560	9	DA023908
40	100.0	561	9	DA957374
41	100.0	562	8	CN264327
42	100.0	562	9	DA542861
43	100.0	566	8	CN264323
44	100.0	566	9	DA178809
45	100.0	567	9	DA027896

ALIGNMENTS

RESULT 1	BF900491	110 bp	mRNA	linear	EST 18-JAN-2001
LOCUS	PM1-MT0198-061200-003-c05	MT0198	Homo sapiens	cdna	mRNA sequence.
DEFINITION	BF900491				
ACCESSION	BF900491.1	GI:12291950			
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 110)				
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7)			3491-3496 (2000)
PUBLISHED	10737800				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-MT0198-061200-003-c05&t3=2000-12-06&t4=1) Seq primer: puc 18 forward High quality sequence start: 6 High quality sequence stop: 110. Location/Qualifiers 1..110 /organism="Homo sapiens" /mol_type="mRNA"				

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/db_xref="taxon:9606"
/dev_stage="Adult"
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/notes="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
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Db 26 GGAGCTAACATCTCCCAAGTC 45

RESULT 2
LOCUS      BF734487      165 bp      mRNA      linear      EST 09-JAN-2001
DEFINITION PM2-AN0089-081100-011-e04 AN0089 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF734487
VERSION     BF734487.1 GI:12059724
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCES  1 (bases 1 to 165)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED    10737800
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM2&t2=PM2-AN0089-
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            High quality sequence stop: 164.
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                /clone_lib="AN0089"
                /note="Organ: amion normal; Vector: puc18; Site_1: SmaI;
                Site_2: SmaI; A mini-library was made by cloning products
                derived from ORSTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the pUC 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
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Db 69 GGAGCTAACATCTCCCAAGTC 88

RESULT 3
LOCUS      T10413/c      222 bp      mRNA      linear      EST 29-NOV-1993
DEFINITION hbc120 Human pancreatic islet Homo sapiens cDNA clone hbc120 5'end,
            mRNA sequence.
ACCESSION  T10413
VERSION     T10413.1 GI:390567
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCES  1 (bases 1 to 222)
AUTHORS    Takeda,J., Yano,H., Eng,S., Zeng,Y. and Bell,G.I.
TITLE      A molecular inventory of human pancreatic islets: sequence analysis
            of 1000 cDNA clones
JOURNAL    Hum. Mol. Genet. 2, 1793-1798 (1993)
PUBMED    7506601
COMMENT    Contact: Bell GI or Takeda J
            HMI
            Univ. of Chicago
            5841 S. Maryland Ave., MC1028, Chicago IL 60637
            Tel: 3127029116
            Fax: 3127020271
            Email: g-bell@uchicago.edu
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                /db_xref="taxon:9606"
                /clones="hbc120"
                /clone_lib="Human pancreatic islet"
                /note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
                I; mRNA was prepared from normal adult human islets. cDNA
                was directionally synthesized from the Xho I in the vector
                to the EcoRI site. cDNA was size fractionated to remove
                sequences <1000 bp in size."

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 222;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
    |||||
Db 27 GGAGCTAACATCTCCCAAGTC 8

RESULT 4
LOCUS      DY178075/c      316 bp      mRNA      linear      EST 02-FEB-2006
DEFINITION 000407BTNA005141HT BTNA Bos taurus cDNA, mRNA sequence.
ACCESSION  DY178075
VERSION     DY178075.1 GI:86382175
KEYWORDS   EST.
SOURCE     Bos taurus (cattle)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.

```

```

REFERENCE
AUTHORS 1 (bases 1 to 316)
          McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
          Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
          Hagmann,L., Lee,R., Hein,W., Johnstone,P., Macbool,N., McMahon,C.,
          McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
          Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
          Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
          Ackinson,P.
TITLE    AgResearch, Genesis and Primary Industry Victoria Bovine EST
         project
JOURNAL  Unpublished (2006)
COMMENT  Contact: Macbool N
         AgResearch Ltd.
         Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
         Mosgiel, New Zealand
         Email: nauman.macbool@agresearch.co.nz.

FEATURES
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         Wayne Hein on 27/01/00"

ORIGIN
Query Match 100.0%; Score 20; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
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Db 277 GGAGCTAACATCTCCAAGTC 258

RESULT 5
LOCUS CN264306/c 324 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700600020922 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN264306
VERSION CN264306.1 GI:47280720
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 324)
          Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
          Li,X., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
          Lebkowski,J and Stanton,L.W
          Transcriptome characterization elucidates signaling networks that
          control human ES cell growth and differentiation
          Nat. Biotechnol. 22 (6), 707-716 (2004)
          15146197
          Contact: Brandenberger R
          Regenerative Medicine
          Geron Corporation
          230 Constitution Drive, Menlo Park, CA 94025, USA
          Tel: 650 473 8658
          Fax: 650 473 7760
          Email: rbrandenberger@geron.com
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          /db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
    |||||
Db 78 GGAGCTAACATCTCCAAGTC 59

RESULT 6
LOCUS BE184816 326 bp mRNA linear EST 22-JUN-2000
DEFINITION QV4-HT0691-270400-186-g04 HT0691 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE184816
VERSION BE184816.1 GI:8664000
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 326)
          Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
          Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
          Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
          Brunstein,A., deOliveira,P.S., Bucher,P., Jorgeneel,C.V.,
          O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and
          Simpson,A.J.
          Shotgun sequencing of the human transcriptome with ORF expressed
          sequence tags
          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
          10737800
          Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome
          Project. This entry can be seen in the following URL
          (http://www.ludwig.org.br/scripts/gethtml2.pl?tti=&t2=QV4-HT0691-270
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          Seq primer: puc 18 forward
          High quality sequence start: 9
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              /dev_stage="Adult"
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              Site 2: SmaI; A mini-library was made by cloning products
              derived from ORESTES PCR (U.S. Letters Patent application
              No. 196.716 - Ludwig Institute for Cancer Research)
              profiles into the pUC 18 vector. Reverse transcription of
              tissue mRNA and cDNA amplification were performed under
              low stringency conditions."

ORIGIN
Query Match 100.0%; Score 20; DB 7; Length 326;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
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/notes="oligo dT primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

1 (bases 1 to 316)
 McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
 Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
 Hagmann,L., Lee,R., Hein,W., Johnstone,P., Macbool,N., McMahon,C.,
 McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
 Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
 Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
 Ackinson,P.

AgResearch, Genesis and Primary Industry Victoria Bovine EST
 project
 Unpublished (2006)
 Contact: Macbool N
 AgResearch Ltd.
 Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
 Mosgiel, New Zealand
 Email: nauman.macbool@agresearch.co.nz.

Location/Qualifiers
 1..316
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="Tonsil"
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/notes="Vector: pBK-CMV; Bovine tonsil cDNA library derived
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 Wayne Hein on 27/01/00"

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 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 277 GGAGCTAACATCTCCAAGTC 258

RESULT 5

LOCUS CN264306/c 324 bp mRNA linear EST 16-MAY-2004
 DEFINITION 1700600020922 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN264306
 VERSION CN264306.1 GI:47280720
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

1 (bases 1 to 324)
 Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
 Li,X., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
 Lebkowski,J and Stanton,L.W
 Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 15146197

JOURNAL

PUBMED

COMMENT

Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
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FEATURES

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QY 1 GGAGCTAACATCTCCAAGTC 20

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McCracken, J., Stelwagen, K., Parr, V., Singh, K., Whitley, J., Nicholas, K., Savin, K., Mather, A., McPartlan, H., Whitley, J., Wells, M., Bowman, P., Goddard, M., Langford, C., McSwan, J. and Atkinson, P.
AgResearch, Genesis and Primary Industry Victoria Bovine EST project
Unpublished (2006)
Contact: Magbool N
AgResearch Ltd.
Invermay Agricultural Centre, Puddle Alley, Private Bag 50034, Moesiel, New Zealand
Email: nauman.magbool@agresearch.co.nz.

TITLE
AgResearch, Genesis and Primary Industry Victoria Bovine EST project
JOURNAL
Unpublished (2006)
COMMENT
Contact: Magbool N
AgResearch Ltd.
Invermay Agricultural Centre, Puddle Alley, Private Bag 50034, Moesiel, New Zealand
Email: nauman.magbool@agresearch.co.nz.

FEATURES
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
D56430/c
LOCUS
D56430
DEFINITION
HUM428804B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA Clone GEN-428E04 5', mRNA sequence.
ACCESSION
D56430
VERSION
D56430.1 GI:971035
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 400)
AUTHORS
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
Fujiwara et al. (1995)
Unpublished (1995)
TITLE
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 kagauno Kawauchi-cho, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 193 GGAGCTAACATCTCCAAAGTC 174

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AW800395/c
LOCUS
MR2-UM0061-050400-105-a08 UM0061 Homo sapiens cDNA, mRNA sequence.
DEFINITION
AW800395
ACCESSION
AW800395.1 GI:7852265
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 421)
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.P., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
TITLE
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR2-UM0061-050400-105-a08&t3=2000-04-05&t4=1)
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High quality sequence start: 20
High quality sequence stop: 420.
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ORIGIN
Query Match 100.0%; Score 20; DB 7; Length 421;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 278 GGAGCTAACATCTCCAAAGTC 259

RESULT 12
BE696421
LOCUS
BE696421
DEFINITION
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ACCESSION
BE696421


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from ORSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGCTAACATCTCCAAGTC 20
Db 225 GGAGCTAACATCTCCAAGTC 206

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Search completed: May 21, 2006, 22:31:08
Job time : 2226.5 secs

ORIGIN

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Db 33 GGAGCTAACATCTCCAAGTC 52

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RESULT 15

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DEFINITION HS_3025_A2_C03 MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plates=3025 Col=6 Row=E, genomic survey
            sequence.
ACCESSION  AQ805950
VERSION    AQ805950.1 GI:5723212
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 453)
            Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
            Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
            Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
            10449764
            Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 3025 row: E column: 6
            Seq primer: M13 Reverse
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            High quality sequence stop: 453.

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Run on: May 21, 2006, 21:18:10 ; Search time 79.5 Seconds
(without alignments)
470.719 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 GGAGCTAACATCTCCAAGTC 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
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- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
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- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	20	100.0	2770	3	US-09-949-016-1518	Sequence 1518, Ap
C 3	20	100.0	3229	3	US-09-919-039-148	Sequence 148, Appl
C 4	20	100.0	3678	3	US-09-380-662-22	Sequence 22, Appl
C 5	20	100.0	3678	3	US-09-959-873B-19	Sequence 19, Appl
C 6	20	100.0	3678	3	US-10-028-158-22	Sequence 22, Appl
C 7	20	100.0	3736	3	US-08-480-473B-1	Sequence 1, Appli
C 8	20	100.0	3736	3	US-08-915-213-1	Sequence 1, Appli
C 9	20	100.0	3736	3	US-09-148-547-1	Sequence 1, Appli
C 10	20	100.0	3736	3	US-09-235-217-1	Sequence 1, Appli
C 11	20	100.0	3736	3	US-09-383-581-1	Sequence 1, Appli
C 12	20	100.0	3736	7	PCT-US96-10251-1	Sequence 218, Appl
C 13	20	100.0	3933	3	US-09-949-016-218	Sequence 13260, A
C 14	20	100.0	18120	3	US-09-949-016-13260	Sequence 11960, A
C 15	20	100.0	56714	3	US-09-949-016-11960	Sequence 11960, A
C 16	18.4	92.0	2481	3	US-10-101-816-1	Sequence 1, Appli
C 17	16.8	84.0	96	2	US-07-648-796A-22	Sequence 22, Appl
C 18	16.8	84.0	393	2	US-07-648-796A-12	Sequence 12, Appl
C 19	16.8	84.0	600	3	US-09-385-982-258	Sequence 258, Appl
C 20	16.8	84.0	1131	2	US-07-648-796A-14	Sequence 14, Appl
C 21	16.8	84.0	2313	2	US-07-648-796A-16	Sequence 16, Appl
C 22	16.8	84.0	2400	2	US-07-648-796A-15	Sequence 15, Appl
C 23	16.8	84.0	10697	3	US-09-949-016-13112	Sequence 13112, A

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25	16.8	84.0	12537	3	US-09-195-940-4	Sequence 4, Appli
26	16.8	84.0	12537	3	US-09-562-466-4	Sequence 4, Appli
C 27	16.4	82.0	321022	3	US-09-949-016-11852	Sequence 11852, A
C 28	16.4	82.0	321022	3	US-09-949-016-14166	Sequence 14166, A
C 29	16	80.0	601	3	US-09-949-016-25790	Sequence 25790, A
C 30	16	80.0	601	3	US-09-949-016-134364	Sequence 134364, A
C 31	16	80.0	24263	3	US-09-949-016-12138	Sequence 12138, A
C 32	16	80.0	24317	3	US-09-949-016-15503	Sequence 15503, A
C 33	15.8	79.0	526	5	US-09-974-300-1390	Sequence 1380, Ap
C 34	15.8	79.0	1509	3	US-09-949-016-3113	Sequence 3113, Ap
C 35	15.8	79.0	3135	5	US-09-984-429-313	Sequence 313, App
C 36	15.8	79.0	3135	5	US-09-984-429-388	Sequence 388, App
C 37	15.8	79.0	72504	3	US-09-949-016-14855	Sequence 14855, A
C 38	15.8	79.0	304533	3	US-09-949-016-15371	Sequence 15371, A
C 39	15.8	79.0	304533	3	US-09-949-016-15372	Sequence 15372, A
C 40	15.8	79.0	786431	3	US-09-751-389-3	Sequence 3, Appli
C 41	15.4	77.0	45842	3	US-09-949-016-16914	Sequence 16914, A
C 42	15.2	76.0	485	3	US-09-621-976-1099	Sequence 1099, Ap
C 43	15.2	76.0	508	3	US-09-621-976-15430	Sequence 15430, A
C 44	15.2	76.0	517	3	US-09-621-976-10337	Sequence 10337, A
C 45	15.2	76.0	601	3	US-09-949-016-151307	Sequence 151307, A

ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09967388
; Patent No. 6838430
; GENERAL INFORMATION:
; APPLICANT: JEFFEREY M. ARBEIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; TITLE OF INVENTION: WOUND HEALING
; FILE REFERENCE: UC077.001A
; CURRENT APPLICATION NUMBER: US/09/967,388
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: HUMAN
US-09-967-388-3

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Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1727 GGAGCTAACATCTCCAAGTC 1708

RESULT 2
US-09-949-016-1518/c
; Sequence 1518, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1518
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; TYPE: DNA
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US-09-949-016-1518

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-919-039-148/c
; Sequence 148, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 148
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1250434CB1
US-09-919-039-148

Query Match 100.0%; Score 20; DB 3; Length 3229;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1958 GGAGCTAACATCTCCCAAGTC 1939

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US-09-380-662-22/c
; Sequence 22, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
LOCATION: (29) .. (2509)

; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1518

Query Match 100.0%; Score 20; DB 3; Length 2770;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
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DB 811 GGAGCTAACATCTCCCAAGTC 792

RESULT 3
US-09-919-039-148/c
; Sequence 148, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 148
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1250434CB1
US-09-919-039-148

Query Match 100.0%; Score 20; DB 3; Length 3229;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
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DB 1958 GGAGCTAACATCTCCCAAGTC 1939

RESULT 4
US-09-380-662-22/c
; Sequence 22, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
LOCATION: (29) .. (2509)

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; LOCATION: (29)..(2509)
US-10-028-158-22

Query Match      100.0%; Score 20; DB 3; Length 3678;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 7
US-08-480-473B-1/c
; Sequence 1, Application US/08480473B
; Patent No. 5882914
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,473B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3736 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-480-473B-1

Query Match      100.0%; Score 20; DB 2; Length 3736;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 8
US-08-915-213-1/c
; Sequence 1, Application US/08915213
; Patent No. 6020462
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
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; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,213
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3736 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-915-213-1

Query Match      100.0%; Score 20; DB 3; Length 3736;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 9
US-09-148-547-1/c
; Sequence 1, Application US/09148547
; Patent No. 6124131
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
; FILE REFERENCE: 07265/151001
; CURRENT APPLICATION NUMBER: US/09/148,547
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(2509)
US-09-148-547-1

Query Match      100.0%; Score 20; DB 3; Length 3736;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 10
US-09-235-217-1/c
; Sequence 1, Application US/09235217
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Patent No. 6222018
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,217
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-235-217-1

Query Match 100.0%; Score 20; DB 3; Length 3736;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
DB 1719 GGAGCTAACATCTCCAAAGTC 1700

RESULT 11
US-09-383-581-1/c
; Sequence 1, Application US/09383581
; Patent No. 6562799
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: JHU1500-1
; CURRENT APPLICATION NUMBER: US/09/383,581
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/148,547
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29) ... (2509)
US-09-383-581-1

Query Match 100.0%; Score 20; DB 3; Length 3736;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
DB 1719 GGAGCTAACATCTCCAAAGTC 1700

RESULT 12
PCT-US96-10251-1/c
; Sequence 1, Application PC/TUS9610251
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10251
; FILING DATE: 06-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3736 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US96-10251-1

Query Match 100.0%; Score 20; DB 7; Length 3736;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
DB 1719 GGAGCTAACATCTCCAAAGTC 1700

RESULT 13
US-09-949-016-218/c
; Sequence 218, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218
; LENGTH: 3933
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-218

Query Match 100.0%; Score 20; DB 3; Length 3933;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 1955 GGAGCTAACATCTCCAAAGTC 1936

RESULT 14
US-09-949-016-13260/c
; Sequence 13260, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13260
; LENGTH: 18120
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13260

Query Match 100.0%; Score 20; DB 3; Length 18120;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 8653 GGAGCTAACATCTCCAAAGTC 8634

RESULT 15
US-09-949-016-11960/c
; Sequence 11960, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11960
; LENGTH: 56714

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11960

Query Match 100.0%; Score 20; DB 3; Length 56714;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 47248 GGAGCTAACATCTCCAAAGTC 47229

Search completed: May 21, 2006, 21:20:58
Job time : 82.5 secs

GenCore version 5.1.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:21:21 ; Search time 823 Seconds
(without alignments)
298.606 Million cell updates/sec

Title: US-10-766-185-4
Perfect score: 20
Sequence: 1 ggagctaacatctccaagtc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10J_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10K_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 2	20	100.0	20	8	US-10-766-185-4	Sequence 4, Appli
C 3	20	100.0	60	3	US-09-908-975-6413	Sequence 6413, Ap
C 4	20	100.0	2481	3	US-09-922-958-3	Sequence 3, Appli
C 5	20	100.0	2481	8	US-10-384-339C-38	Sequence 38, Appli
C 6	20	100.0	2487	10	US-10-450-763-20859	Sequence 20859, A
C 7	20	100.0	2517	3	US-09-967-388-3	Sequence 3, Appli
C 8	20	100.0	2528	7	US-10-204-724-2	Sequence 2, Appli
C 9	20	100.0	2861	7	US-10-264-049-431	Sequence 431, App
C 10	20	100.0	3180	7	US-10-425-784-3	Sequence 3, Appli
C 11	20	100.0	3229	3	US-09-919-039-148	Sequence 148, App
C 12	20	100.0	3229	6	US-10-208-408-22	Sequence 22, Appli
C 13	20	100.0	3229	6	US-10-084-817-113	Sequence 113, App
C 14	20	100.0	3229	7	US-10-247-671-19	Sequence 19, Appli
C 15	20	100.0	3551	8	US-10-304-126-13	Sequence 13, Appli
C 16	20	100.0	3551	9	US-10-719-370A-13	Sequence 13, Appli
C 17	20	100.0	3678	6	US-10-028-158-22	Sequence 22, Appli

C 18	20	100.0	3678	9	US-10-901-583-19	Sequence 19, Appli
C 19	20	100.0	3678	10	US-10-007-255-3	Sequence 3, Appli
C 20	20	100.0	3678	13	US-11-043-493-22	Sequence 22, Appli
C 21	20	100.0	3736	7	US-10-423-419-1	Sequence 1, Appli
C 22	20	100.0	3736	10	US-10-831-380-1	Sequence 1, Appli
C 23	20	100.0	3812	9	US-10-699-557-3	Sequence 3, Appli
C 24	20	100.0	3927	3	US-09-833-790-231	Sequence 231, App
C 25	20	100.0	3933	7	US-10-172-118-625	Sequence 625, App
C 26	20	100.0	3933	7	US-10-388-360-309	Sequence 309, App
C 27	20	100.0	3933	8	US-10-342-887-625	Sequence 625, App
C 28	20	100.0	3933	8	US-10-407-807-1	Sequence 1, Appli
C 29	20	100.0	3933	8	US-10-304-126-4	Sequence 4, Appli
C 30	20	100.0	3933	9	US-10-719-370A-4	Sequence 4, Appli
C 31	20	100.0	3933	9	US-10-719-370A-133	Sequence 133, App
C 32	20	100.0	3933	9	US-10-848-646-3	Sequence 3, Appli
C 33	20	100.0	3933	10	US-10-956-157-643	Sequence 643, App
C 34	20	100.0	3933	10	US-10-494-800-59	Sequence 59, Appli
C 35	20	100.0	3933	16	US-11-288-720-1	Sequence 1, Appli
C 36	20	100.0	3958	9	US-10-699-557-2	Sequence 2, Appli
C 37	20	100.0	4162	10	US-10-450-763-20862	Sequence 20862, A
C 38	20	100.0	4656	6	US-10-044-090-284	Sequence 284, App
C 39	20	100.0	4727	7	US-10-115-987B-12	Sequence 12, Appli
C 40	20	100.0	4740	7	US-10-115-987B-13	Sequence 13, Appli
C 41	20	100.0	10355	7	US-10-204-724-4	Sequence 4, Appli
C 42	20	100.0	57500	9	US-10-719-370A-11	Sequence 11, Appli
C 43	20	100.0	57501	8	US-10-304-126-11	Sequence 11, Appli
C 44	18.4	92.0	2481	6	US-10-101-816-1	Sequence 1, Appli
C 45	18.4	92.0	2481	9	US-10-854-483-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-766-185-3/c
; Sequence 3, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
; APPLICANT: Yoon, Heejeong
; APPLICANT: Ahn, Chang Ho
; APPLICANT: Lee, Young Bok
; APPLICANT: Mao, Lingjun
; APPLICANT: Jiang, Xiaoming
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
; FILE REFERENCE: REX 7034
; CURRENT APPLICATION NUMBER: US/10766,185
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
US-10-766-185-3

Query Match	100.0%	Score	20;	DB	8;	Length	20;
Best Local Similarity	100.0%	Pred. No.	4.4;				
Matches	20;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						

Oy 1 GGAGCTAACATCTCCAGTC 20
|||||
Db 20 GGAGCTAACATCTCCAGTC 1

RESULT 2
US-10-766-185-4
; Sequence 4, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
; APPLICANT: Yoon, Heejeong
; APPLICANT: Ahn, Chang Ho
; APPLICANT: Lee, Young Bok
; APPLICANT: Mao, Lingjun

APPLICANT: Jiang, Xiaoming
TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
FILE REFERENCE: REX 7034
CURRENT APPLICATION NUMBER: US/10/766.185
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 20
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: antisense oligonucleotide
US-10-766-185-4

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
|||||
Db 1 GGAGCTAACATCTCCAAGTC 20

RESULT 3
US-09-908-975-6413/c
Sequence 6413, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6413
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-6413

Query Match 100.0%; Score 20; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.9; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
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Db 51 GGAGCTAACATCTCCAAGTC 32

RESULT 4
US-09-922-958-3/c
Sequence 3, Application US/09922958
Patent No. US20020048794A1
GENERAL INFORMATION:
APPLICANT: POELLINGER, Lorenz
APPLICANT: PEREIRA, Teresa
APPLICANT: RUAS, Jorge
TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACT
TITLE OF INVENTION: THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
FILE REFERENCE: 3743/49008
CURRENT APPLICATION NUMBER: US/09/922,958
CURRENT FILING DATE: 2001-08-07

PRIOR APPLICATION NUMBER: US 60/223,480
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 2481
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2478)
US-09-922-958-3

Query Match 100.0%; Score 20; DB 3; Length 2481;
Best Local Similarity 100.0%; Pred. No. 7.3; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
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Db 1691 GGAGCTAACATCTCCAAGTC 1672

RESULT 5
US-10-384-339C-38/c
Sequence 38, Application US/10384339C
Publication No. US20040175703A1
GENERAL INFORMATION:
APPLICANT: Kreutzer, Roland
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET
FILE REFERENCE: 20200/2002
CURRENT APPLICATION NUMBER: US/10/384,339C
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: PCT/EP02/00152
PRIOR FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: DE 10100586.5
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: DE 10155280.7
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 2481
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
TITLE: HIF-alpha
PATENT DOCUMENT NUMBER: U22431
US-10-384-339C-38

Query Match 100.0%; Score 20; DB 8; Length 2481;
Best Local Similarity 100.0%; Pred. No. 7.3; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
|||||
Db 1691 GGAGCTAACATCTCCAAGTC 1672

RESULT 6
US-10-450-763-20859/c
Sequence 20859, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631

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; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 20859
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (574)..(2487)
; OTHER INFORMATION: 9% homologous to Homo sapiens 06-JUN-1995 Human hypoxia
; OTHER INFORMATION: Inducible factor-1 alpha cDNA, accession number T45937_cdl, Smith-
US-10-450-763-20859

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Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 2487;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
Db 1697 GGAGCTAACATCTCCAAAGTC 1678

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```

RESULT 7
US-09-967-388-3/c
; Sequence 3, Application US/09967388
; Publication No. US20030103956A1
; GENERAL INFORMATION:
; APPLICANT: JEFFEREY M. ARBEIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; FILE REFERENCE: UC077.001A
; CURRENT APPLICATION NUMBER: US/09/967,388
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: HUMAN
US-09-967-388-3

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Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 2517;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
Db 1727 GGAGCTAACATCTCCAAAGTC 1708

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RESULT 8
US-10-724-724-2/c
; Sequence 2, Application US/10204724
; Publication No. US20030180740A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, John Alan
; TITLE OF INVENTION: DIFFERENTIAL EXPRESSION SCREENING METHOD
; FILE REFERENCE: 5326200200
; CURRENT APPLICATION NUMBER: US/10/204,724
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: PCT/GB01/00758
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: GB 0018679.1
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: GB 0004197.0
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2528
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-204-724-2

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Query Match
Best Local Similarity 100.0%; Score 20; DB 7; Length 2528;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
Db 1718 GGAGCTAACATCTCCAAAGTC 1699

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```

RESULT 9
US-10-264-049-431/c
; Sequence 431, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 431
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2853)..(2853)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-431

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Query Match
Best Local Similarity 100.0%; Score 20; DB 7; Length 2861;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
Db 841 GGAGCTAACATCTCCAAAGTC 822

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RESULT 10
US-10-425-784-3/c
; Sequence 3, Application US/10425784
; Publication No. US20040009591A1
; GENERAL INFORMATION:
; APPLICANT: Comer, Allen
; APPLICANT: Hoffmann, Michael
; APPLICANT: Allen-Hoffmann, Lynn
; TITLE OF INVENTION: Keratinocytes Expressing Exogenous Angiogenic Growth Factors
; FILE REFERENCE: STRATA-08110
; CURRENT APPLICATION NUMBER: US/10/425,784
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 60/376,488
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3180
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-425-784-3

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Query Match      100.0%; Score 20; DB 7; Length 3180;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
DB 1955 GGAGCTAACATCTCCAAGTC 1936

RESULT 11
US-09-919-039-148/c
; Sequence 148, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 148
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CB1
US-09-919-039-148

Query Match      100.0%; Score 20; DB 3; Length 3229;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
DB 1958 GGAGCTAACATCTCCAAGTC 1939

RESULT 12
US-10-208-408-22/c
; Sequence 22, Application US/10208408
; Publication No. US20030096272A1
; GENERAL INFORMATION:
; APPLICANT: Schebye, Xiao Min
; TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
; FILE REFERENCE: PA-0048-1 US
; CURRENT APPLICATION NUMBER: US/10/208,408
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,868
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030096272A1 1250434CB1
US-10-208-408-22

Query Match      100.0%; Score 20; DB 6; Length 3229;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
DB 1958 GGAGCTAACATCTCCAAGTC 1939
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RESULT 13
US-10-084-817-113/c
; Sequence 113, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 113
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1250434CB1
US-10-084-817-113

Query Match      100.0%; Score 20; DB 6; Length 3229;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
DB 1958 GGAGCTAACATCTCCAAGTC 1939

RESULT 14
US-10-247-671-19/c
; Sequence 19, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1250434CB1
US-10-247-671-19

Query Match      100.0%; Score 20; DB 7; Length 3229;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
DB 1958 GGAGCTAACATCTCCAAGTC 1939

RESULT 15
US-10-304-126-13/c
; Sequence 13, Application US/10304126
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; Publication No. US20040101858A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HYPOXIA-INDUCIBLE FACTOR 1 ALPHA EXPRESSION
; FILE REFERENCE: PTS-0070
; CURRENT APPLICATION NUMBER: US/10/304,126
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 13
; LENGTH: 3551
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)...(2236)
US-10-304-126-13

Query Match      100.0%; Score 20; DB 8; Length 3551;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GGAGCTAACATCTCCAGTC 20
        |||||
Db      1719 GGAGCTAACATCTCCAGTC 1700

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Search completed: May 21, 2006, 21:48:56
Job time : 824 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:33:45 ; Search time 13.5 Seconds
(without alignments)
104.527 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggaagtaacatctccaagtc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	77.0	25	7	US-11-217-529-23140 Sequence 23140, A
2	15.4	77.0	1080	7	US-11-217-529-1559 Sequence 1559, Ap
3	15.2	76.0	25	7	US-11-217-529-107428 Sequence 107428, A
4	15.2	76.0	590	6	US-10-488-619-2776 Sequence 2776, Ap
5	15.2	76.0	630	7	US-11-217-529-3916 Sequence 3916, Ap
6	15.2	76.0	1080	7	US-11-217-529-77549 Sequence 77549, A
7	14.8	74.0	2823	7	US-11-217-529-4032 Sequence 4032, Ap
8	14.8	74.0	6075	7	US-11-217-529-3047 Sequence 3047, Ap
9	14.4	72.0	2397	7	US-11-217-529-254 Sequence 254, App
10	14.2	71.0	432	7	US-11-217-529-2519 Sequence 2519, Ap
11	14.2	71.0	537	7	US-11-301-554-1175 Sequence 1175, Ap
12	14.2	71.0	1710	7	US-11-024-544A-58 Sequence 58, Appl
13	14.2	71.0	1710	7	US-11-190-750-35 Sequence 35, Appl
14	14.2	71.0	5105	7	US-11-024-544A-82 Sequence 82, Appl
15	14.2	71.0	5105	7	US-11-190-750-63 Sequence 63, Appl
16	14.2	71.0	5105	7	US-11-264-784-157 Sequence 157, App
17	14.2	71.0	6457	7	US-11-264-784-117 Sequence 117, App
18	14.2	71.0	7145	7	US-11-264-784-121 Sequence 121, App
19	14.2	71.0	7323	7	US-11-024-544A-168 Sequence 168, App
20	14.2	71.0	7323	7	US-11-024-545-68 Sequence 68, Appl
21	14.2	71.0	7323	7	US-11-251-466-53 Sequence 53, Appl
22	14.2	71.0	7323	7	US-11-254-173-61 Sequence 61, Appl
23	14.2	71.0	7323	7	US-11-264-784-140 Sequence 140, App
24	14.2	71.0	7822	7	US-11-024-544A-144 Sequence 144, App
25	14.2	71.0	7822	7	US-11-264-784-153 Sequence 153, App

ALIGNMENTS

RESULT 1

US-11-217-529-23140
; Sequence 23140, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23140
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-23140

Query Match 77.0%; Score 15.4; DB 7; Length 25;
Best Local Similarity 94.1%; Pred. No. 6;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGTC 20

|||||
Db 5 GCTAAGATCTCCAAGTC 21

RESULT 2

US-11-217-529-1559
; Sequence 1559, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

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; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1559
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1559

Query Match      77.0%; Score 15.4; DB 7; Length 1080;
Best Local Similarity 94.1%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCTAATCTCTCCAAGTC 20
      ||||| ||||| ||||| |||||
DB     1030 GCTAATCTCTCCAAGTC 1046

RESULT 3
US-11-217-529-107428
; Sequence 107428, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107428
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-107428

Query Match      76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 7.7;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGAGCTAACATCTCCAAGTC 20
      ||||| ||||| ||||| |||||
DB      5 GGTGCTAAGATCACCACGTC 24

RESULT 4
US-10-488-619-2776/c
; Sequence 2776, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2776
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2776
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Query Match      76.0%; Score 15.2; DB 6; Length 590;
Best Local Similarity 85.0%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGAGCTAACATCTCCAAGTC 20
      ||||| ||||| ||||| |||||
DB     539 GGAGATGACATGTCCAAGTC 520

RESULT 5
US-11-217-529-3916
; Sequence 3916, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3916
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3916

Query Match      76.0%; Score 15.2; DB 7; Length 630;
Best Local Similarity 85.0%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGAGCTAACATCTCCAAGTC 20
      ||||| ||||| ||||| |||||
DB      61 GAAGCTATATATCACCACGTC 80

RESULT 6
US-11-217-529-77549
; Sequence 77549, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77549
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77549

Query Match      76.0%; Score 15.2; DB 7; Length 1080;
Best Local Similarity 85.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGAGCTAACATCTCCAAGTC 20
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US-11-217-529-254
; Sequence 254, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 254
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-254

Query Match 72.0%; Score 14.4; DB 7; Length 2397;
Best Local Similarity 93.8%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gap

Qy 3 AGCTAACATCTCCAG 18
Db 581 ATCTAACATCTCCAG 596

RESULT 10
US-11-217-529-2519
; Sequence 2519, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2519
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2519

Query Match 71.0%; Score 14.2; DB 7; Length 432;
Best Local Similarity 84.2%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gap

Qy 1 GGAGCTAACATCTCCAAGT 19
Db 202 GAAGCTAACATCTCAAGT 220

RESULT 11
US-11-301-554-1175/c
; Sequence 1175, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.

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; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; PRIOR FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1175
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1175

Query Match 71.0%; Score 14.2; DB 7; Length 537;
Best Local Similarity 84.2%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGT 19
Db 499 GGAGCTGACTTCGCCAAGT 481

RESULT 12
US-11-024-544A-58
; Sequence 58, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1175
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; TYPE: DNA
; ORGANISM: Yarrowia lipolytica
US-11-024-544A-58

Query Match 71.0%; Score 14.2; DB 7; Length 1710;
Best Local Similarity 84.2%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAAAGTC 20
Db 404 GAGCTAACGTCCCAAGTC 422

RESULT 13
US-11-190-750-35
; Sequence 35, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Yarrowia lipolytica
US-11-190-750-35

Query Match 71.0%; Score 14.2; DB 7; Length 1710;
Best Local Similarity 84.2%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAAAGTC 20
Db 404 GAGCTAACGTCCCAAGTC 422

RESULT 14
US-11-024-544A-82/c
; Sequence 82, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82
; LENGTH: 5105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid plv13
; NAME/KEY: misc feature
; LOCATION: (4446)..(4446)
; OTHER INFORMATION: n is a, c, g, or t
US-11-024-544A-82
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Query Match 71.0%; Score 14.2; DB 7; Length 5105;
Best Local Similarity 84.2%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAAAGTC 20
|||||||
Db 3692 GAGCTAACGTCCACAAAGTC 3674

RESULT 15
US-11-190-750-63/c
; Sequence 63, Application US/11190750
; Publication No. US20060094088a1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 5105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pLV13
; NAME/KEY: misc feature
; LOCATION: (4446)..(4446)
; OTHER INFORMATION: n is a, c, g, or t
US-11-190-750-63

Query Match 71.0%; Score 14.2; DB 7; Length 5105;
Best Local Similarity 84.2%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAAAGTC 20
|||||||
Db 3692 GAGCTAACGTCCACAAAGTC 3674

Search completed: May 21, 2006, 21:34:20
Job time : 14.5 secs

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Please also a standard search of SEQ ID NOS: 2 and 4.

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Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search NA# _____
AA# _____
S/L: _____
Oligomer: _____
Encode/Transl: _____
Structure #: _____
Text: _____
Inventor: _____
Litigation: _____

Vendors and cost where applicable STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____